

GenCore version 5.1.4.P5\_4578  
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OM protein - protein search, using sw model

Run on: March 24, 2003, 16:06:20 ; Search time 12 seconds

(without alignment)  
902.110 Million cell updates/sec

Title: US-09-988-971-2

Perfect score: 261  
Sequence: 1 MSLSPRRKSLSPSLSSSV.....RESLFFYSLNDEAVSLDA 261

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : SwissProt\_40.\*

Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	9	3.4	504	1	BUX_HUMAN
2	9	3.4	552	1	SRCI_PROME
3	8	3.1	151	1	YVTS_WHEAT
4	8	3.1	217	1	GRAP_HUMAN
5	8	3.1	217	1	GRB2_CHICK
6	8	3.1	217	1	GRB2_HUMAN
7	8	3.1	217	1	GRB2_MOUSE
8	8	3.1	217	1	GRB2_XENLA
9	8	3.1	461	1	P55G_BOVIN
10	8	3.1	461	1	P55G_HUMAN
11	8	3.1	461	1	P55G_MOUSE
12	8	3.1	503	1	HCK_RAT
13	8	3.1	504	1	HCK_MACPA
14	8	3.1	507	1	LCK_CHICK
15	8	3.1	511	1	LYN_HUMAN
16	8	3.1	511	1	LYN_MOUSE
17	8	3.1	511	1	LYN_RAT
18	8	3.1	517	1	FGF_MOUSE
19	8	3.1	524	1	HCK_MOUSE
20	8	3.1	526	1	HCK_HUMAN
21	8	3.1	529	1	FGF_HUMAN
22	8	3.1	533	1	FGF_MOUSE
23	8	3.1	1819	1	GCPE_HUMAN
24	8	3.1	137	1	NS51_SOYAN
25	7	2.7	157	1	RSVR_COTJA
26	7	2.7	157	1	COAE_RHIME
27	7	2.7	251	1	COX2_MARPO
28	7	2.7	269	1	TRIM_CANPA
29	7	2.7	293	1	IC66_HUMAN
30	7	2.7	301	1	RNHL_MOUSE
31	7	2.7	345	1	OGG1_HUMAN
32	7	2.7	355	1	FKB8_HUMAN
33	7	2.7	355	1	FKB8_MOUSE

34	7	2.7	365	1	SOXB_RHOSO
35	7	2.7	394	1	HMPA_VIRBA
36	7	2.7	473	1	ZF38_HUMAN
37	7	2.7	506	1	HERIN_ANAP
38	7	2.7	544	1	YES_XIPHE
39	7	2.7	555	1	ZF38_MOUSE
40	7	2.7	594	1	NPA1_MOUSE
41	7	2.7	597	1	ZF37_HUMAN
42	7	2.7	610	1	RCK2_YEAST
43	7	2.7	631	1	VG42_HAEIN
44	7	2.7	653	1	PABF_SCHRO
45	7	2.7	702	1	SPB1_ARATH
46	7	2.7	702	1	SPB1_ARATH
47	7	2.7	711	1	SPB2_ARATH
48	7	2.7	743	1	Z267_HUMAN
49	7	2.7	754	1	TBP6_YEAST
50	7	2.7	760	1	OCT1_XENLA
51	7	2.7	787	1	ITB6_MOUSE
52	7	2.7	788	1	ITB6_HUMAN
53	7	2.7	816	1	ATX1_HUMAN
54	7	2.7	941	1	YBPA_SALTY
55	7	2.7	946	1	YBPA_YEAST
56	7	2.7	1117	1	YN96_YEAST
57	7	2.7	1426	1	CUT2_MOUSE
58	7	2.7	1565	1	CUT2_HUMAN
59	7	2.7	1606	1	MYM1_MOUSE
60	7	2.7	1833	1	ZEP2_HUMAN
61	7	2.7	2842	1	APC_RAT
62	7	2.7	2843	1	APC_HUMAN
63	7	2.7	2845	1	APC_MOUSE
64	6	2.3	52	1	RL40_CHLRE
65	6	2.3	53	1	RL40_ORYSA
66	6	2.3	82	1	CSGA_BACSU
67	6	2.3	86	1	Y425_TREPA
68	6	2.3	89	1	DBHB_METMA
69	6	2.3	90	1	TEGP_HSVB
70	6	2.3	91	1	DBHC_METMA
71	6	2.3	96	1	CH10_BUCMP
72	6	2.3	96	1	REV_SIVAM
73	6	2.3	106	1	IATP_MOUSE
74	6	2.3	107	1	IATP_RAT
75	6	2.3	108	1	END4_THENE
76	6	2.3	114	1	RLA1_HUMAN
77	6	2.3	114	1	RLA1_RAT
78	6	2.3	120	1	RI8B_AERPE
79	6	2.3	122	1	VFID_ECOLI
80	6	2.3	123	1	ELI2_PHYCR
81	6	2.3	126	1	G8_HUMAN
82	6	2.3	128	1	U384_HSVMG
83	6	2.3	130	1	YJ84_YEAST
84	6	2.3	133	1	ATPE_BACHD
85	6	2.3	134	1	ATPE_RUMAL
86	6	2.3	135	1	YABO_METUA
87	6	2.3	137	1	MSCI_YERPE
88	6	2.3	137	1	TFX_METTH
89	6	2.3	137	1	TFX_METTH
90	6	2.3	141	1	NDK_AERPE
91	6	2.3	144	1	YOR5_KLEPN
92	6	2.3	145	1	VG46_BPMU
93	6	2.3	147	1	VH83_SYNY3
94	6	2.3	148	1	YCT9_YEAST
95	6	2.3	155	1	PAZX_HUMAN
96	6	2.3	158	1	FXSA_ECOLI
97	6	2.3	163	1	LCA_RAT
98	6	2.3	165	1	YOR3_EAV
99	6	2.3	165	1	CGHB_HUMAN
100	6	2.3	166	1	REL2_PANTR

P54997	rhodococcus
P40609	vibrio para
O9Y566	homo sapien
P37693	anabena sp
P27447	xiphophorus
Q07231	mus musculus
P97459	mus musculus
O9Y643	homo sapien
P38623	saccharomyc
P44236	haemophilus
P31209	schizosacch
O96164	arabidopsis
O82475	braesica ju
O23141	arabidopsis
O14586	homo sapien
P40328	saccharomyc
P16143	xenopus lae
O92019	mus musculus
P18564	homo sapien
P54253	homo sapien
P37434	salmonella
P38250	saccharomyc
P53753	saccharomyc
P70298	mus musculus
O14529	homo sapien
O62234	mus musculus
P31629	homo sapien
P70478	rattus norv
P25054	homo sapien
O61315	mus musculus
P14695	chlamydomon
P35296	oryza sativ
P54379	baecillus su
O83440	treponema p
O9Y116	neisseria m
P30025	simian hep
O9Y130	neisseria m
O51831	buchnera ap
P36339	simian immu
O35143	mus musculus
Q03344	rattus norv
O86954	thermoplas
P05386	homo sapien
P19944	rattus norv
O9Y851	aeropyrum p
P76511	escherichia
P41803	phytophor
O9Y846	homo sapien
Q05102	marek's dis
P47151	saccharomyc
O9Y646	baecillus ha
O50143	ruminococcu
O58480	methanococ
O82183	yersinia pe
O27001	methanobact
P56811	methanobact
O9Y850	aeropyrum p
O48451	klebsiella
O9Y133	bacterioph
P73602	synchocyst
P25629	saccharomyc
O15496	homo sapien
P37147	escherichia
P00714	rattus norv
P28893	equine arte
P01233	homo sapien
P51455	pan troglod

## ALIGNMENTS

RESULT 1

BLK\_HUMAN  
ID BLK\_HUMAN STANDARD; PRT; 504 AA.  
AC P51451; O16291;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Tyrosine-protein kinase BLK (EC 2.7.1.112) (B lymphocyte kinase) (p55-BLK).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
[1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95148218; PubMed=7822795;  
RA Islam K.B., Rabbani H., Larsson C., Sanders R., Smith C.I.;  
RT "Molecular cloning, characterization, and chromosomal localization of a human lymphoid tyrosine kinase related to murine Blk.";  
RL J. Immunol. 154:1265-1272(1995).  
[2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=95148218; PubMed=7845672;  
RA Drebin J.A., Hartzell S.W., Griffin C., Campbell M.J.,  
RT "Molecular cloning and chromosomal localization of the human homologue of a B-lymphocyte specific protein tyrosine kinase (blk).";  
RL Oncogene 10:477-486(1995).  
CC -1- FUNCTION: BLK MAY FUNCTION IN A SIGNAL TRANSDUCTION PATHWAY THAT IS RESTRICTED TO B LYMPHOID CELLS.  
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.  
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC SUBFAMILY.  
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
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CC -----  
DR EMBL: Z33938; CAA8365.1; -;  
DR EMBL: S76617; AAB33265.1; -;  
DR HSSP: P16277; BLK.  
DR Genew; HGNC:1057; BLK.  
DR MIM; 191305; -;  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR000980; SH2.  
DR InterPro: IPR001452; SH3.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF00017; SH2; 1.  
DR Pfam: PF00018; SH3; 1.  
DR Pfam: PF00069; pkinase; 1.  
DR PRINTS: PRO0401; SH2DOMAIN.  
DR PRINTS: PRO0452; SH3DOMAIN.  
DR PRINTS: PRO0109; TYRKINASE.  
DR ProDom: PD000001; Euk\_pkinase; 1.  
DR ProDom: PD000066; SH3; 1.  
DR ProDom: PD000093; SH2; 1.  
DR SMART: SM00252; SH2; 1.  
DR SMART: SM00326; SH3; 1.  
DR SMART: SM00219; TYRK; 1.  
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE: PS00109; PROTEIN KINASE TYR; FALSE-NEG.  
DR PROSITE: PS50011; PROTEIN KINASE\_DOM; 1.  
DR PROSITE: PS50001; SH2; 1.  
DR PROSITE: PS50002; SH3; 1.  
KW Tyrosine-protein kinase; Phosphorylation; Transferase; ATP-binding; Myristate; SH2 domain; SH3 domain.

FT INIT MET 0 0 BY SIMILARITY.  
FT LIPID 1 1 MYRISTATE (BY SIMILARITY).  
FT DOMAIN 57 117 SH3.  
FT DOMAIN 123 219 SH2.  
FT DOMAIN 240 493 PROTEIN KINASE.  
FT NP\_BIND 246 254 ATP (BY SIMILARITY).  
FT BINDING 268 268 ATP (BY SIMILARITY).  
FT ACT\_SITE 359 359 BY SIMILARITY.  
FT MOD\_RES 388 388 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
FT CONFLICT 286 286 M -> V (IN REF. 2).  
FT CONFLICT 406 406 I -> Y (IN REF. 2).  
SQ SEQUENCE 504 AA; 57607 MW; 5BBD5F50EC370C8 CRC64;  
  
Query Match 3.4%; Score 9; DB 1; Length 504;  
Best Local Similarity 100.0%; Pred. No. 0.78;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Oy 165 TPSPLOALV 173  
Db 193 TPSPLOALV 201  
  
RESULT 2  
SRC1\_DROME STANDARD; PRT; 552 AA.  
ID SRC1\_DROME  
AC P00528; O18372; Q9VZA2;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Tyrosine-protein kinase Src64b (EC 2.7.1.112).  
GN SRC64b OR SRC1 OR CG7524.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=7227;  
[1]  
RP SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND DEVELOPMENTAL STRGE.  
RX MEDLINE=86028179; PubMed=2996778;  
RA Simon M.A., Drees B., Kornberg T., Bishop J.M.;  
RT "The nucleotide sequence and the tissue-specific expression of Drosophila c-src".  
RL Cell 42:831-840(1985).  
[2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berkeley;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brannon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miles G.L.G., Araki J.F., Agbayani A., An H.-J., Andrews-Ffannoch C., Balwin D., Ballaw R.M., Basu A., Baxendale U., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Bernan B.P., Brokstein P., Brottier P., Borkova D., Botchan M.R., Bouck J., Brockstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Duan-Rocha S., Dunkov B.C., Dunn P., Dodson K., Doup I.E., Downes M., Dugan-Rocha S., Dinkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferriere S., Fleischmann W., Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaeser K., Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kotika C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Matei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Mishaeva N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy W., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svrtkac R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 Science 287:2185-2195(2000).  
 RN [3]  
 RP SEQUENCE OF 249-552 FROM N.A.  
 RX MEDLINE=84082064; PubMed=6317185;  
 RA Hoffmann F.M., Fresco L.D., Hoffman-Palk H., Shilo B.-Z.;  
 RT "Nucleotide sequences of the *Drosophila* src and abl homologs:  
 RT conservation and variability in the src family oncogenes.";  
 RL Cell 35:393-401(1983).  
 RN [4]  
 RP SEQUENCE OF 410-461 FROM N.A.  
 RX MEDLINE=98401146; PubMed=9731193;  
 RA Oates A.C., Wollberg P., Achen W.G., Wilks A.F.;  
 RT "Sampling the genomic pool of protein tyrosine kinase genes using the  
 RT polymerase chain reaction with genomic DNA.";  
 RL Biochem. Biophys. Res. Commun. 249:660-667(1998).  
 CC -1- FUNCTION: May play a role in the development of neural tissue and  
 CC smooth muscle.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- TISSUE SPECIFICITY: After the first 8 hr of development,  
 CC accumulates almost exclusively in neural tissues, such as the  
 CC brain, ventral nerve chord, and eye-antennal disks, and in  
 CC differentiating smooth muscle.  
 CC -1- DEVELOPMENTAL STAGE: Abundant in embryos and pupae, rare in larvae  
 CC and adults.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC  
 CC SUPRANITY.  
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
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 CC -----  
 DR EMBL: M11917; AAA28913.1; -;  
 DR EMBL: AE003481; AAF47922.1; -;  
 DR EMBL: K01043; AAA28489.1; -;  
 DR EMBL: AJ002919; CAA05754.1; -;  
 DR PIR: A00634; TRFS.  
 DR HSP: P11362; TRFS.  
 DR FLYbase: Fegm0003501; Src64B.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR000980; SH2.  
 DR InterPro: IPR001452; SH3.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR InterPro: IPR001245; Tyr\_pkinase.  
 DR Pfam: PF00017; SH2; 1.  
 DR Pfam: PF00018; SH3; 1.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PRINTS: PRO0401; SH2DOMAIN.  
 DR PRINTS: PRO0452; SH3DOMAIN.  
 DR PRINTS: PRO0109; TYRKINASE.  
 DR ProDom: PD000001; Euk\_pkinase; 1.  
 DR ProDom: PD000066; SH3; 1.  
 DR ProDom: PD000093; SH2; 1.  
 DR SMART: SM00252; SH2; 1.  
 DR SMART: SM00326; SH3; 1.  
 DR SMART: SM00326; SH3; 1.

DR SMART: SM00220; S\_TKC; 1.  
 DR SMART: SM00219; Tyrc; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS50001; SH2; 1.  
 DR PROSITE: PS50002; SH3; 1.  
 KW Kinase; Tyrosine-protein kinase; Proto-oncogene; Phosphorylation;  
 KW Transferase; ATP-binding; SH3 domain; SH2 domain;  
 KW Developmental protein.  
 FT DOMAIN 95 156  
 FT SH3.  
 FT DOMAIN 162 259  
 FT SH2.  
 FT DOMAIN 284 537  
 FT SH2.  
 FT NP\_BIND 290 298  
 FT ATP (BY SIMILARITY).  
 FT BINDING 312 312  
 FT ACT\_SITE 404 404  
 FT MOD\_RES 434 434  
 FT CONFLICT 102 102  
 FT CONFLICT 261 263  
 FT CONFLICT 261 263  
 FT CONFLICT 266 269  
 FT CONFLICT 272 272  
 FT CONFLICT 272 272  
 FT CONFLICT 286 287  
 FT CONFLICT 290 290  
 FT CONFLICT 293 293  
 FT CONFLICT 316 316  
 FT CONFLICT 366 366  
 FT CONFLICT 373 373  
 FT CONFLICT 384 385  
 FT CONFLICT 389 390  
 FT CONFLICT 393 393  
 FT CONFLICT 400 400  
 FT CONFLICT 406 407  
 FT CONFLICT 435 435  
 FT CONFLICT 460 460  
 FT CONFLICT 471 471  
 FT CONFLICT 484 484  
 FT CONFLICT 507 507  
 FT CONFLICT 536 536  
 FT SEQUENCE 552 AA; 63002 MW; 4A63CF4F16562864 CRC64;  
 SQ  
 Query Match 3.4%; Score 9; DB 1; Length 552;  
 Best local Similarity 100.0%; Pred. No. 0.85;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 165 TPSPSLQALV 173  
 DB 233 TPSPSLQALV 241  
 RESULT 3  
 TWIS WHEAT STANDARD; PRT; 151 AA.  
 ID TWIS WHEAT  
 AC P14723;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical 16 kDa protein in middle repetitive insertion sequence  
 DE WIS1.  
 OS Triticum aestivum (Wheat).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Triticum.  
 OK NCBI\_TaxID=4565;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Chinese Spring;  
 RX MEDLINE=89364725; PubMed=2549380;  
 RA Martensen R.A., Baulcombe D.C.;  
 RT "An unusual wheat insertion sequence (WIS1) lies upstream of an  
 RT alpha-amylase gene in hexaploid wheat, and carries a 'minisatellite'  
 RT array.";  
 RL Mol. Gen. Genet. 217:401-410(1989).  
 CC -----

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DR EMBL; X15870; CAJ33860.1; -.  
 DR PIR; S10084; S10084.  
 KW Transposable element; Hypothetical protein.  
 SQ SEQUENCE 151 AA; 15950 MW; 3BA30BD31EC6742 CRC64;

Query Match 3.1%; Score 8; DB 1; Length 151;  
 Best Local Similarity 100.0%; Pred. No. 2.4;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 LPSPLSS 18  
 DB 22 LPSPLSS 29

RESULT 4  
 ID GRAP HUMAN STANDARD; PRT; 217 AA.  
 AC Q13588  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE GRB2-related adaptor protein.  
 GN GRAP.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96218119; PubMed=8647802;  
 RA Feng G.-S., Ouyang Y.-B., Hu D.-P., Shi Z.-Q., Gentz R., Ni J.;  
 RT "Grp is a novel SH3-SH2-SH3 adaptor protein that couples tyrosine  
 RT kinases to the Ras pathway."  
 RL J. Biol. Chem. 271:12129-12132(1996).

CC -1- FUNCTION: COUPLES SIGNALS FROM RECEPTOR AND CYTOPLASMIC TYROSINE  
 CC KINASES TO THE RAS SIGNALING PATHWAY.  
 CC -1- SUBUNIT: ASSOCIATES THROUGH ITS SH2 DOMAIN WITH LIGAND-ACTIVATED  
 CC RECEPTORS FOR STEM CELL FACTOR (KIT) AND ERYTHROPOIETIN (EPOR).  
 CC ALSO FORMS A STABLE COMPLEX WITH THE BCR-ABL ONCOPROTEIN. GRAP IS  
 CC ASSOCIATED WITH THE RAS GUANINE NUCLEOTIDE EXCHANGE FACTOR SOS1,  
 CC PRIMARILY THROUGH ITS N-TERMINAL SH3 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
 CC -1- SIMILARITY: BELONGS TO THE GRB2 / SEM-5 / DRK FAMILY.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; U52518; AAC50541.1; -.  
 DR HSSP; Q60631; IGB0.  
 DR Genew; HGNC:4562; GRAP.  
 DR MIM; 604330; -.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 2.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR ProDom; PD000066; SH3; 2.  
 DR ProDom; PD000093; SH2; 1.  
 DR SMART; SM00252; SH2; 1.

DR SMART; SM00326; SH3; 2.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 2.  
 KW SH2 domain; SH3 domain; Repeat.  
 FT DOMAIN 1 58 SH3 1.  
 FT DOMAIN 60 152 SH2.  
 FT DOMAIN 156 215 SH3 2.  
 SQ SEQUENCE 217 AA; 25336 MW; 09FECF3BAC0FAF8 CRC64;

Query Match 3.1%; Score 8; DB 1; Length 217;  
 Best Local Similarity 100.0%; Pred. No. 3.4;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 GAFLIRS 123  
 DB 81 GAFLIRS 88

RESULT 5  
 ID GRB2\_CHICK STANDARD; PRT; 217 AA.  
 AC Q07883;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Growth factor receptor-bound protein 2 (GRB2 adapter protein)  
 DE (SH2/SH3 adapter GRB2) (ASH protein).  
 GN GRB2.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OX Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=94085795; PubMed=8262390;  
 RA Masenius V.-M., Merilainen J., Lento V.-P.;  
 RT "Sequence of a chicken cDNA encoding a GRB2 protein."  
 RL Gene 134:289-300(1993).

CC -1- FUNCTION: ASSOCIATES WITH ACTIVATED TYROSINE-PHOSPHORYLATED EGF  
 CC RECEPTORS AND PDGF RECEPTORS VIA ITS SH2 DOMAIN. GRB2 ALSO  
 CC ASSOCIATES TO OTHER CELLULAR TYROSINE-PHOSPHORYLATED PROTEINS SUCH  
 CC AS IRS-1, SHC AND LNK. PROBABLY VIA THE CONCERTED ACTION OF BOTH  
 CC ITS SH2 AND SH3 DOMAINS. IT ALSO SEEMS TO INTERACT WITH RAS  
 CC IN THE SIGNALING PATHWAY LEADING TO DNA SYNTHESIS. BINDS TO AND  
 CC TRANSLOCATES THE GUANINE NUCLEOTIDE EXCHANGE FACTORS SOS.  
 CC -1- FUNCTION: PROBABLY REPRESENTS A REGULATORY SUBUNIT OF DOWNSTREAM  
 CC SIGNALING MOLECULES WHOSE ACTIVITY IS MODULATED BY RECEPTOR  
 CC BINDING. A 55 KDA PHOSPHOPROTEIN OF UNKNOWN FUNCTION WHICH BINDS  
 CC TO GRB2 IN RESPONSE TO GROWTH FACTOR STIMULATION COULD BE A  
 CC DOWNSTREAM SIGNALING MOLECULE CANDIDATE.  
 CC -1- TISSUE SPECIFICITY: WIDE TISSUE AND CELL DISTRIBUTION.  
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE GRB2 / SEM-5 / DRK FAMILY.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; L19258; AAA16318.1; -.  
 DR PIR; J10664; J10664.  
 DR HSSP; P29354; IGR1.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 2.  
 DR PRINTS; PR00452; SH3DOMAIN.

DR PRODOM: PD0000066; SH3; 2.  
 DR PRODOM: PD0000093; SH2; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 2.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 2.  
 KM SH2 domain; SH3 domain; Repeat.  
 FT DOMAIN 1 58 SH3 1.  
 FT DOMAIN 60 152 SH2 1.  
 FT DOMAIN 156 215 SH3 2.  
 SQ SEQUENCE 217 AA; 25076 MW; DDC9A84BCDC52859 CRC64;  
 Query Match 3.1%; Score 8; DB 1; Length 217;  
 Best Local Similarity 100.0%; Pred. No. 3.4;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 116 GAFIRES 123  
 DB 81 GAFIRES 88  
 RESULT 6  
 GRB2 HUMAN STANDARD; PRT; 217 AA.  
 ID GRB2 HUMAN STANDARD; PRT; 217 AA.  
 AC P29354; O63057; Q14450;  
 DT 01-DEC-1992 (Rel. 24, Created)  
 DT 01-DEC-1992 (Rel. 24, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Growth factor receptor-bound protein 2 (GRB2 adapter protein)  
 DE (SH2/SH3 adapter GRB2) (ASH protein).  
 GN GRB2 OR ASH.  
 OS Homo sapiens (Human), and  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606, 10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Human; TISSUE=Brain;  
 RX MEDLINE=92354060; PubMed=1322798;  
 RA Lowenstein E.J., Daly R.J., Batzer A.G., Li W., Margolis B.,  
 RA Lammers R., Ullrich A., Skolnik E.Y., Bar-Sagi D., Schlessinger J.;  
 RT "The SH2 and SH3 domain-containing protein GRB2 links receptor  
 RT tyrosine kinases to ras signaling.";  
 RL Cell 70:431-442(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Human, and Rat; TISSUE=Brain, and Lung;  
 RX MEDLINE=93028395; PubMed=1184039;  
 RA Matluka K., Yamakawa A., Shibata M., Takenawa T.;  
 RT "Cloning of ASH, a ubiquitous protein composed of one Src homology  
 RT region (SH) 2 and two SH3 domains, from human and rat cDNA  
 RT libraries.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 89:9015-9019(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
 RC SPECIES=Rat; STRAIN=Miscar; TISSUE=Brain;  
 RX MEDLINE=95293967; PubMed=775428;  
 RA Watanabe K., Fukuchi T., Hosoya H., Shirasawa T., Matsuda K.,  
 RA Miki H., Takenawa T.;  
 RT "Splicing isoforms of rat Ash/Grb2. Isolation and characterization of  
 RT the cDNA and genomic DNA clones and implications for the  
 RT physiological roles of the isoforms.";  
 RL J. Biol. Chem. 270:13733-13739(1995).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOPFORM GRB3-3).  
 RC SPECIES=Human; TISSUE=Placenta;  
 RX MEDLINE=94233382; PubMed=8178156;  
 RA Fath I., Schweighofer F., Rey I., Multon M.C., Boiziau J.,  
 RA Duchesne M., Tocque B.;  
 RT "Cloning of a Grb2 isoform with apoptotic properties.";  
 RL Science 264:971-974(1994).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Human; TISSUE=Epidermis;  
 RX MEDLINE=99162407; PubMed=10051406;  
 RA Boeckmann H., Gehring S., Jarois W.;  
 RT "The gene structure of the human growth factor bound protein GRB2.";  
 RL Genomics 56:203-207(1999).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Human; TISSUE=Lymph;  
 RA Strauberg R.;  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP ASSOCIATION WITH IRS-1.  
 RX MEDLINE=93259135; PubMed=8389384;  
 RA Tobe K., Matluka K., Tamemoto H., Ueki K., Kaburagi Y., Asai S.,  
 RA Noguchi T., Matsuda M., Tanaka S., Hattori S., Fukui Y., Akanuma Y.,  
 RA Yazaki Y., Takenawa T., Kawakami T.;  
 RT "Insulin stimulates association of insulin receptor substrate-1 with  
 RT the protein abundant Src homology/growth factor receptor-bound  
 RT protein 2.";  
 RL J. Biol. Chem. 268:11167-11171(1993).  
 RN [8]  
 RP ASSOCIATION WITH IRS-1 AND SHC.  
 RX MEDLINE=93259135; PubMed=8491186;  
 RA Skolnik E.Y., Lee C.-H., Batzer A., Vicentini L.M., Zhou M., Daly R.,  
 RA Myers M.J. Jr., Backer J.M., Ullrich A., White M.F., Schlessinger J.;  
 RT "The SH2/SH3 domain-containing protein GRB2 interacts with tyrosine-  
 RT phosphorylated IRS1 and Shc: implications for insulin control of ras  
 RT signaling.";  
 RL EMBO J. 12:1929-1936(1993).  
 RN [9]  
 RP STRUCTURE BY NMR OF 1-56.  
 RX MEDLINE=97280795; PubMed=9135122;  
 RA Wittekind M., Mapelli C., Lee V., Goldfarb V., Friedrichs M.S.,  
 RA Meyers C.A., Mueller L.;  
 RT "Solution structure of the Grb2 N-terminal SH3 domain complexed with  
 RT a ten-residue peptide derived from SOS: direct refinement against  
 RT NOE, J-couplings and 1H and 13C chemical shifts.";  
 RL J. Mol. Biol. 267:933-952(1997).  
 RN [10]  
 RP STRUCTURE BY NMR OF 60-158.  
 RX MEDLINE=96387228; PubMed=8794768;  
 RA Thornton K.H., Mueller W.T., McConnell P., Zhu G., Saliel A.R.,  
 RA Thanabal V.;  
 RT "Nuclear magnetic resonance solution structure of the growth factor  
 RT receptor-bound protein 2 Src homology 2 domain.";  
 RL Biochemistry 35:11852-11864(1996).  
 RN [11]  
 RP STRUCTURE BY NMR OF 53-163.  
 RA Senior M.M., Frederick A.F., Black S., Murgolo N.J., Perkins L.M.,  
 RA Wilson O., Snow M.E., Wang Y.-S.;  
 RT "The three-dimensional solution structure of the Src homology domain-2  
 RT of the growth factor receptor-bound protein-2.";  
 RL J. Biomol. NMR 11:153-164(1998).  
 RN [12]  
 RP STRUCTURE BY NMR OF 159-215.  
 RX MEDLINE=95187706; PubMed=7881903;  
 RA Kohda D., Terasawa H., Ichikawa S., Ogura K., Hatanaka H.,  
 RA Mandiyan V., Ullrich A., Schlessinger J., Inagaki F.;  
 RT "Solution structure and ligand-binding site of the carboxy-terminal  
 RT SH3 domain of GRB2.";  
 RL Structure 2:1029-1040(1994).  
 RN [13]  
 RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS).  
 RX MEDLINE=95232505; PubMed=716522;  
 RA Maigani S., Gulloteau J.P., Fromage N., Arnoux B., Becquart J.,  
 RA Duchesne A.;  
 RT "Crystal structure of the mammalian Grb2 adaptor.";  
 RL Science 268:291-295(1995).  
 RN [14]  
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 56-153.  
 RX MEDLINE=98308003; PubMed=9642078;  
 RA Rahuel J., Garcia-Echeverria C., Furet P., Straus A., Caravatti G.,

RA Fretz H., Schoepfer J., Gay B.;  
 RT "Structural basis for the high affinity of amino-aromatic SH2  
 RT phosphopeptide ligands.";  
 RT J. Mol. Biol. 279:1013-1022(1998).  
 RN [15]  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 49-163.  
 RA MEDLINE=99192587; PubMed=10090780;  
 RA Etmeayer P., France D., Gonnardides J., Jarosinski M., Martin M.-S.,  
 RA Rondeau J.-M., Sabio M., Topiol S., Weidmann B., Zurini M., Bahr K.W.;  
 RT "Structural and conformational requirements for high-affinity binding  
 RT to the SH2 domain of Grb2(1).";  
 RT J. Med. Chem. 42:971-980(1999).  
 RN [16]  
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 57-152.  
 RA MEDLINE=99344016; PubMed=10395476;  
 RA Furet P., Garcia-Echeverria C., Gay B., Schoepfer J., Zeller M.,  
 RA Rahuel J.;  
 RT "Structure-based design, synthesis, and X-ray crystallography of a  
 RT high-affinity antagonist of the Grb2-SH2 domain containing an  
 RT asparagine mimetic.";  
 RT J. Med. Chem. 42:2358-2363(1999).  
 CC -1- FUNCTION: ASSOCIATES WITH ACTIVATED TYROSINE-PHOSPHORYLATED EGF  
 CC RECEPTORS AND PDGF RECEPTORS VIA ITS SH2 DOMAIN. GRB2 ALSO  
 CC ASSOCIATES TO OTHER CELLULAR TYROSINE-PHOSPHORYLATED PROTEINS SUCH  
 CC AS IRS-1, SHC AND LNK. PROBABLY VIA THE CONCERTED ACTION OF BOTH  
 CC ITS SH2 AND SH3 DOMAINS. IT ALSO SEEMS TO INTERACT WITH RAS  
 CC IN THE SIGNALING PATHWAY LEADING TO DNA SYNTHESIS. BINDS TO AND  
 CC TRANSLOCATES THE GUANINE NUCLEOTIDE EXCHANGE FACTORS SOS.  
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 CC TO GRB2 IN RESPONSE TO GROWTH FACTOR STIMULATION COULD BE A  
 CC DOWNSTREAM SIGNALING MOLECULE CANDIDATE.  
 CC -1- FUNCTION: ISOFORM GRB3-3 DOES NOT BIND TO PHOSPHORYLATED EPIDERMAL  
 CC GROWTH FACTOR RECEPTOR (EGFR) BUT INHIBITS EGF-INDUCED  
 CC TRANSACTIVATION OF A RAS-RESPONSIVE ELEMENT. GRB3-3 ACTS AS A  
 CC DOMINANT NEGATIVE PROTEIN OVER GRB2 AND BY SUPPRESSING  
 CC PROLIFERATIVE SIGNALS. MAY TRIGGER ACTIVE PROGRAMMED CELL DEATH.  
 CC -1- ALTERNATIVE PRODUCTS: A NUMBER OF FORMS ARE PRODUCED BY  
 CC ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: WIDE TISSUE AND CELL DISTRIBUTION.  
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE GRB2 / SEM-5 / DRK FAMILY.  
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 CC -----  
 DR EMBL: M66995; AAA58448.1; -;  
 DR EMBL: X62853; CAA44664.1; -;  
 DR EMBL: X62853; CAA44665.1; -;  
 DR EMBL: D48846; BAA08645.1; -;  
 DR EMBL: L29511; AAC37549.1; -;  
 DR EMBL: AF063618; AAC72075.1; -;  
 DR EMBL: AF063614; AAC72075.1; JOINED.  
 DR EMBL: AF063615; AAC72075.1; JOINED.  
 DR EMBL: AF063616; AAC72075.1; JOINED.  
 DR EMBL: AF063617; AAC72075.1; JOINED.  
 DR EMBL: BC000631; AAH00631.1; -;  
 DR PIR: A43321; A43321.  
 DR PIR: S26050; S26050.  
 DR PDB: 1GRI; 08-MAR-96.  
 DR PDB: 1GFC; 31-AUG-94.  
 DR PDB: 1GPD; 31-AUG-94.  
 DR PDB: 1GHU; 27-JAN-97.  
 DR PDB: 1TZE; 07-JUL-97.  
 DR PDB: 1PHS; 17-JUN-98.  
 DR PDB: 1BM2; 05-AUG-98.

DR PDB: 1BM2; 29-JUL-98.  
 DR PDB: 1ZEP; 30-MAR-99.  
 DR PDB: 1CJ1; 22-DEC-99.  
 DR Genew; HGNC:4566; GRB2.  
 Query Match 3.1%; Score 8; DB 1; Length 217;  
 Best Local Similarity 100.0%; Pred. No. 3.4;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 116 GARLINES 123  
 Db 81 GARLINES 88  
 RESULT 7  
 GRB2\_MOUSE STANDARD; PRT; 217 AA.  
 AC Q60631; Q61240;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Growth factor receptor-bound protein 2 (GRB2 adapter protein)  
 DE (SH2/SH3 adapter GRB2).  
 GN GRB2.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RX MEDLINE=93360985; PubMed=7689150;  
 RA Shen K., Bustelo X.R., Pawson T., Barbacid M.;  
 RT "Molecular cloning of the mouse grb2 gene: differential interaction  
 RT of the Grb2 adaptor protein with epidermal growth factor and nerve  
 RT growth factor receptors.";  
 RL Mol. Cell. Biol. 13:5500-5512(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM GRB3-3).  
 RC STRAIN=BALB/c;  
 RX Tanaka S.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP STRUCTURE BY NMR OF 1-59.  
 RX MEDLINE=97280795; PubMed=9135122;  
 RA Wittekand M., Mepelli C., Lee V., Goldfarb V., Friedrichs M.S.,  
 RA Meyers C.A., Mueller L.;  
 RT "Solution structure of the Grb2 N-terminal SH3 domain complexed with  
 RT a ten-residue peptide derived from SOS: direct refinement against  
 RT NOES, J-couplings and 1H and 13C chemical shifts.";  
 RL J. Mol. Biol. 267:933-952(1997).  
 CC -1- FUNCTION: ASSOCIATES WITH ACTIVATED TYROSINE-PHOSPHORYLATED EGF  
 CC RECEPTORS AND PDGF RECEPTORS VIA ITS SH2 DOMAIN. GRB2 ALSO  
 CC ASSOCIATES TO OTHER CELLULAR TYROSINE-PHOSPHORYLATED PROTEINS SUCH  
 CC AS IRS-1, SHC AND LNK. PROBABLY VIA THE CONCERTED ACTION OF BOTH  
 CC ITS SH2 AND SH3 DOMAINS. IT ALSO SEEMS TO INTERACT WITH RAS  
 CC IN THE SIGNALING PATHWAY LEADING TO DNA SYNTHESIS. BINDS TO AND  
 CC TRANSLOCATES THE GUANINE NUCLEOTIDE EXCHANGE FACTORS SOS.  
 CC -1- FUNCTION: PROBABLY REPRESENTS A REGULATORY SUBUNIT OF DOWNSTREAM  
 CC SIGNALING MOLECULES WHOSE ACTIVITY IS MODULATED BY RECEPTOR  
 CC BINDING. A 55 KDA PHOSPHOPROTEIN OF UNKNOWN FUNCTION WHICH BINDS  
 CC TO GRB2 IN RESPONSE TO GROWTH FACTOR STIMULATION COULD BE A  
 CC DOWNSTREAM SIGNALING MOLECULE CANDIDATE.  
 CC -1- FUNCTION: ISOFORM GRB3-3 DOES NOT BIND TO PHOSPHORYLATED EPIDERMAL  
 CC GROWTH FACTOR RECEPTOR (EGFR) BUT INHIBITS EGF-INDUCED  
 CC TRANSACTIVATION OF A RAS-RESPONSIVE ELEMENT. GRB3-3 ACTS AS A  
 CC DOMINANT NEGATIVE PROTEIN OVER GRB2 AND BY SUPPRESSING  
 CC PROLIFERATIVE SIGNALS, MAY TRIGGER ACTIVE PROGRAMMED CELL DEATH  
 CC (BY SIMILARITY).  
 CC -1- ALTERNATIVE PRODUCTS: A NUMBER OF FORMS ARE PRODUCED BY  
 CC ALTERNATIVE SPLICING.  
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.

CC -1- SIMILARITY: BELONGS TO THE GRB2 / SEM-5 / DRK FAMILY.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: U07617; AAB40022.1; -  
CC EMBL: D85748; BAA12862.1; -  
CC PDB: 1GBQ; 04-SEP-97.  
CC PDB: 2GBQ; 04-SEP-97.  
CC PDB: 3GBQ; 04-SEP-97.  
CC PDB: 4GBQ; 04-SEP-97.  
CC PDB: 1GBR; 26-JAN-95.  
CC MGD: MGI:95805; Gdb2.  
CC InterPro: IPR000980; SH2.  
CC InterPro: IPR001452; SH3.  
CC Pfam: PF00017; SH2; 1.  
CC Pfam: PF00018; SH3; 2.  
CC PRINTS: PR00401; SH2DOMAIN.  
CC PRINTS: PR00452; SH3DOMAIN.  
CC ProDom: PD000066; SH3; 2.  
CC ProDom: PD000093; SH2; 1.  
CC SMART: SM00252; SH2; 1.  
CC SMART: SM00326; SH3; 2.  
CC PROSITE: PS50001; SH2; 1.  
CC PROSITE: PS50002; SH3; 2.  
CC SH2 domain; SH3 domain; Repeat; Alternative splicing; 3D-structure.  
FT DOMAIN 1 58 SH3 1.  
FT DOMAIN 60 152 SH2.  
FT DOMAIN 156 215 SH3 2.  
FT VARSPLIC 60 100 MISSING (IN ISOFORM GRB3-3).  
SQ SEQUENCE 217 AA; 25238 MW; 97F44FE4B248DDF CRC64;  
  
Query Match 3.1%; Score 8; DB 1; Length 217;  
Best Local Similarity 100.0%; Pred. No. 3.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 116 GAFLIRES 123  
Db 81 GAFLIRES 88  
|||||  
Db 81 GAFLIRES 88  
  
RESULT 8  
ID GRB2\_XENLA STANDARD; PRT; 217 AA.  
AC P87379;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Growth factor receptor-bound protein 2 (GRB2 adapter protein)  
DE (SH2/SH3 adapter GRB2).  
GN GRB2.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
OC Xenopodidae; Xenopus.  
OC NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lu W., Mayer B.J.;  
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: ASSOCIATES WITH ACTIVATED TYROSINE-PHOSPHORYLATED EGF  
CC RECEPTORS AND PDGF RECEPTORS VIA ITS SH2 DOMAIN. GRB2 ALSO  
CC ASSOCIATES TO OTHER CELLULAR TYROSINE-PHOSPHORYLATED PROTEINS SUCH  
CC AS IRS-1, SHC AND LNK; PROBABLY VIA THE COORDINATED ACTION OF BOTH  
CC ITS SH2 AND SH3 DOMAINS. IT ALSO SEEMS TO INTERACT WITH RAS  
CC PROTEIN IN THE SIGNALING PATHWAY LEADING TO DNA SYNTHESIS (BY  
CC SIMILARITY).  
CC -1- FUNCTION: PROBABLY REPRESENTS A REGULATORY SUBUNIT OF DOWNSTREAM

CC SIGNALING MOLECULES WHOSE ACTIVITY IS MODULATED BY RECEPTOR  
CC BINDING. A 55 KDA PHOSPHOPROTEIN OF UNKNOWN FUNCTION WHICH BINDS  
CC TO GRB2 IN RESPONSE TO GROWTH FACTOR STIMULATION COULD BE A  
CC DOWNSTREAM SIGNALING MOLECULE CANDIDATE (BY SIMILARITY).  
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.  
CC -1- SIMILARITY: BELONGS TO THE GRB2 / SEM-5 / DRK FAMILY.  
CC  
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CC  
CC EMBL: U89775; AAB49699.1; -  
CC HSSP: P29354; IGHU.  
CC InterPro: IPR000980; SH2.  
CC InterPro: IPR001452; SH3.  
CC Pfam: PF00017; SH2; 1.  
CC Pfam: PF00018; SH3; 2.  
CC PRINTS: PR00452; SH3DOMAIN.  
CC ProDom: PD000066; SH3; 2.  
CC ProDom: PD000093; SH2; 1.  
CC SMART: SM00252; SH2; 1.  
CC SMART: SM00326; SH3; 2.  
CC PROSITE: PS50001; SH2; 1.  
CC PROSITE: PS50002; SH3; 2.  
CC SH2 domain; SH3 domain; Repeat.  
FT DOMAIN 1 58 SH3 1.  
FT DOMAIN 60 152 SH2.  
FT DOMAIN 156 215 SH3 2.  
SQ SEQUENCE 217 AA; 25104 MW; 1622802ED26CE46A CRC64;  
  
Query Match 3.1%; Score 8; DB 1; Length 217;  
Best Local Similarity 100.0%; Pred. No. 3.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 116 GAFLIRES 123  
Db 81 GAFLIRES 88  
|||||  
Db 81 GAFLIRES 88  
  
RESULT 9  
ID P55G\_BOVIN STANDARD; PRT; 461 AA.  
AC O46404;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Phosphatidylinositol 3-kinase regulatory gamma subunit (PI3-kinase  
DE p85-gamma subunit) (Ptdins-3-kinase p85-gamma) (p55PIK).  
GN PI3KR.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OC NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Adrenal cortex;  
RA Varnai P., Balla T.;  
RT p55gamma, a regulatory subunit of PI 3-kinase from adrenal cortex.";  
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: BINDS TO ACTIVATED (PHOSPHORYLATED) PROTEIN-TYROSINE  
CC KINASES THROUGH ITS SH2 DOMAIN AND REGULATES THEIR KINASE  
CC ACTIVITY. DURING INSULIN STIMULATION, IT ALSO BINDS TO IRS-1.  
CC SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P55 (REGULATORY)  
CC SUBUNIT.  
CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS IN BRAIN AND TESTIS. LOWER  
CC LEVELS IN ADIPOSE TISSUE, KIDNEY, HEART, LUNG AND SKELETAL MUSCLE.  
CC BARELY DETECTABLE IN LIVER AND SPLEEN.

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CC -1- SIMILARITY: BELONGS TO THE PI3K P85 SUBUNIT FAMILY.
CC -1- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF036256; AAB88704.1; -.
DR HSSP: P23727; 2PNB.
DR InterPro: IPR001720; PI3kinase_P85.
DR InterPro: IPR000980; SH2.
DR Pfam: PF00017; SH2; 2.
DR PRINTS: PR00678; PI3KINASEP85.
DR PRINTS: PR00401; SH2DOMAIN.
DR ProDom: PD000093; SH2; 2.
DR SMART: SM00252; SH2; 2.
DR PROSITE: PS50001; SH2; 2.
DR SH2 domain; Repeat; Phosphorylation.
FT DOMAIN 65 160 SH2 1.
FT MOD RES 358 452 SH2 2.
FT MOD RES 341 341 PHOSPHORYLATION (BY SIMILARITY).
SQ SEQUENCE 461 AA; 5438 MW; C5B77282B9A96DAD CRC64;

Query Match 3.1%; Score 8; DB 1; Length 461;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 116 GAFIRES 123
Db 378 GAFIRES 385

RESULT 10
P55G_HUMAN STANDARD; PRT; 461 AA.
ID P55G_HUMAN STANDARD; PRT; 461 AA.
AC Q92569; Q60482;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phosphatidylinositol 3-kinase regulatory gamma subunit (PI3-kinase
DE p85-gamma subunit) (Ptdins-3-kinase p85-gamma) (p55PIK).
GN PIK3R3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Suzuki T.;
RT "Molecular cloning of human p55piK."
RT Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.
RU [2]
RN SEQUENCE FROM N.A. (ISOFORMS 1, 2 AND 3).
RC TISSUE=Fetal brain;
RX MEDLINE=98192526; PubMed=9524259;
RA Dey B.R., Furlanetto R.W., Nisley S.P.;
RT "Cloning of human p55 gamma, a regulatory subunit of
RT phosphatidylinositol 3-kinase, by a yeast two-hybrid library screen
RT with the insulin-like growth factor-1 receptor."
RU Gene 209:175-183(1998).
CC -1- FUNCTION: BINDS TO ACTIVATED (PHOSPHORYLATED) PROTEIN-TYROSINE
CC KINASES THROUGH ITS SH2 DOMAIN AND REGULATES THEIR KINASE
CC ACTIVITY. DURING INSULIN STIMULATION, IT ALSO BINDS TO IRS-1.
CC -1- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
CC SUBUNITS.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS IN BRAIN AND TESTIS. LOWER
CC LEVELS IN ADIPOSE TISSUE, KIDNEY, HEART, LUNG AND SKELETAL MUSCLE.

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CC -1- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
CC -1- SIMILARITY: HIGH, WITH OTHER P85 SUBUNITS, AND WITH P85-ALPHA AND
CC P85-BETA SUBUNITS.
CC -----
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CC -----
DR EMBL: D88532; BA13636.1; -.
DR EMBL: AF028785; AAC39696.1; -.
DR HSSP: P23727; 2PNB.
DR Genew: HGNC:8981; PIK3R3.
DR MIM: 606076; -.
DR InterPro: IPR001720; PI3kinase_P85.
DR InterPro: IPR000980; SH2.
DR Pfam: PF00017; SH2; 2.
DR PRINTS: PR00678; PI3KINASEP85.
DR PRINTS: PR00401; SH2DOMAIN.
DR ProDom: PD000093; SH2; 2.
DR SMART: SM00252; SH2; 2.
DR PROSITE: PS50001; SH2; 2.
DR SH2 domain; Repeat; Phosphorylation; Alternative splicing.
FT DOMAIN 34 44 PRO-RICH.
FT DOMAIN 65 160 SH2 1.
FT DOMAIN 358 452 SH2 2.
FT MOD RES 341 341 PHOSPHORYLATION (BY SIMILARITY).
FT VARSLIC 36 71 MISSING (IN ISOFORM 3).
FT VARSPLIC 256 314 MISSING (IN ISOFORM 2 AND ISOFORM 3).
FT CONFLICT 21 21 F -> L (IN REF. 2).
SQ SEQUENCE 461 AA; 54462 MW; C03CFF22B50B9 CRC64;

Query Match 3.1%; Score 8; DB 1; Length 461;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 116 GAFIRES 123
Db 378 GAFIRES 385

RESULT 11
P55G_MOUSE STANDARD; PRT; 461 AA.
ID P55G_MOUSE STANDARD; PRT; 461 AA.
AC Q64143;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phosphatidylinositol 3-kinase regulatory gamma subunit (PI3-kinase
DE p85-gamma subunit) (Ptdins-3-kinase p85-gamma) (p55PIK).
GN PIK3R3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=95349612; PubMed=7542745;
RA Pons S., Asano T., Glasheen E., Mizalpeix M., Zhang Y., Fisher T.L.,
RA Wiers M.G. Jr., Sun X.J., White M.F.;
RT "The structure and function of p55piK reveal a new regulatory subunit
RT for phosphatidylinositol 3-kinase."
RU Mol. Cell. Biol. 15:4453-4465(1995).
CC -1- FUNCTION: BINDS TO ACTIVATED (PHOSPHORYLATED) PROTEIN-TYROSINE
CC KINASES THROUGH ITS SH2 DOMAIN AND REGULATES THEIR KINASE
CC ACTIVITY. DURING INSULIN STIMULATION, IT ALSO BINDS TO IRS-1.
CC -1- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
CC SUBUNITS.
CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS IN BRAIN AND TESTIS. LOWER

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CC LEVELS IN ADIPOSE TISSUE, KIDNEY, HEART, LUNG AND SKELETAL MUSCLE.
CC BARELY DETECTABLE IN LIVER AND SPLEEN.
CC -1- SIMILARITY: BELONGS TO THE PI3K P85 SUBUNIT FAMILY.
CC -1- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
CC -----
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CC -----
CC EMBL: S79169; AAB34938.1; -.
CC HSSP: P23727; 2PMB.
CC DR MGD; MGI:109277; P1K3r3.
CC DR InterPro: IPR001720; PI3K_kinase_P85.
CC DR InterPro: IPR000980; SH2.
CC DR Pfam: PF00017; SH2; 2.
CC DR PRINTS: PR00678; PI3K_kinase_P85.
CC DR PRINTS: PR00401; SH2DOMAIN.
CC DR ProDom: PD000093; SH2; 2.
CC DR SMART: SM00252; SH2; 2.
CC DR PROSITE: PS50001; SH2; 2.
CC DR SH2 domain; Repeat: Phosphorylation.
CC FT DOMAIN 65 160 SH2 1.
CC FT DOMAIN 358 452 SH2 2.
CC FT MOD RES 341 341 PHOSPHORYLATION.
CC SQ SEQUENCE 461 AA; 54474 MW; 97A01ADDFAC661F CRC64;

Query Match 3.1%; Score 8; DB 1; Length 461;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 GAFLRES 123
Db 378 GAFLRES 385

RESULT 12
HCK_RAT
ID HCK_RAT STANDARD; PRT; 503 AA.
AC P50545; 064647;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase HCK (EC 2.7.1.112) (P56-HCK) (Hemopoietic cell
DE kinase).
GN HCK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=92109719; Pubmed=1764064;
RA Okano Y., Sugimoto Y., Fukuoaka M., Matsui A., Nagata K.I., Nozawa Y.;
RA "Identification of rat cDNA encoding hck tyrosine kinase from
RT megakaryocytes.";
RL Biochem. Biophys. Res. Commun. 181:1137-1144(1991).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Spleen;
RA Vijaya Gouri B.S., Remy V., Kamatkar S., Swarup G.;
RA "Nucleotide sequence of a cDNA coding for rat hck tyrosine kinase and
RT characterization of its gene product.";
RL J. Biosci. 19:117-129(1994).
CC -1- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC
CC RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO
CC CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE
CC DEGRANULATION PROCESS OF NEUTROPHILS.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
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CC -1- SUBCELLULAR LOCATION: Membrane-associated.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
CC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -----
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CC -----
CC EMBL: S74141; AAB20754.1; -.
CC DR EMBL: M83666; AAA4312.1; -.
CC DR EMBL: X62345; CAA44218.1; -.
CC HSSP: P08631; 1BUL.
CC DR InterPro: IPR000719; Euk_pkinase.
CC DR InterPro: IPR000980; SH2.
CC DR InterPro: IPR001452; SH3.
CC DR InterPro: IPR001245; Tyr_pkinase.
CC DR Pfam: PF00017; SH2; 1.
CC DR Pfam: PF00018; SH3; 1.
CC DR Pfam: PF00069; pkinase; 1.
CC DR PRINTS: PR00401; SH2DOMAIN.
CC DR PRINTS: PR00452; SH3DOMAIN.
CC DR PRINTS: PR00109; TYRKINASE.
CC DR ProDom: PD000001; Euk_pkinase; 1.
CC DR ProDom: PD000066; SH3; 1.
CC DR ProDom: PD000093; SH2; 1.
CC DR SMART: SM00252; SH2; 1.
CC DR SMART: SM00326; SH3; 1.
CC DR SMART: SM00219; Tyrc; 1.
CC DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
CC DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
CC DR PROSITE: PS50011; SH2; 1.
CC DR PROSITE: PS50002; SH3; 1.
CC KW Transferrase; Tyrosine-protein kinase; Phosphorylation; ATP-binding;
KW Myristate; SH2 domain; SH3 domain.
GN MYRISTATE; SH2 domain; SH3 domain.
FT DOMAIN 55 115 SH3.
FT DOMAIN 121 218 SH2.
FT DOMAIN 239 492 PROTEIN_KINASE.
FT NP_BIND 245 253 ATP (BY SIMILARITY).
FT BINDING 267 267 ATP (BY SIMILARITY).
FT ACT SITE 358 358 BY SIMILARITY.
FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
FT MOD RES 388 388 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CONFLICT 51 51 F -> V (IN REF. 2).
FT CONFLICT 205 205 K -> R (IN REF. 2).
FT CONFLICT 306 306 I -> T (IN REF. 2).
SQ SEQUENCE 503 AA; 57016 MW; A1PCLF3F0B82FE73 CRC64;

Query Match 3.1%; Score 8; DB 1; Length 503;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 GSYSLSVR 135
Db 155 GSYSLSVR 162

RESULT 13
HCK_MACPA
ID HCK_MACPA STANDARD; PRT; 504 AA.
AC Q95M30;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase HCK (EC 2.7.1.112) (P56-HCK) (Hemopoietic cell
DE kinase).
GN HCK.
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OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RF SEQUENCE FROM N.A.
RA Picard C.;
RL Thesis (2001), University of Marseille, France.
CC -1- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE PC
CC RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO
CC CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE
CC DEGRANULATION PROCESS OF NEUTROPHILS (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Membrane-associated (By similarity).
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
CC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -----
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CC -----
DR EMBL: AJ320181; CAC44031.1; -
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR Pfam: PF00069; pkinase; 1.
DR Prodom: PD000001; Euk_pkinase; 1.
DR Prodom: PD000066; SH3; 1.
DR Prodom: PD000093; SH2; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50001; SH2; 1.
DR PROSITE: PS50002; SH3; 1.
KW Transferase: Tyrosine-protein kinase; Phosphorylation; ATP-binding;
KW Myristate; SH2 domain; SH3 domain.
FT DOMAIN 56 116
FT DOMAIN 122 219
FT NP BIND 240 493
FT NP BIND 246 254
FT BINDING 268 268
FT ACT SITE 359 359
FT LIPID 2 2
FT MOD RES 389 389
FT SEQUENCE 504 AA; 57096 MW; 53829322D2DE3423 CRC64;
SQ
Query Match 3.1%; Score 8; DB 1; Length 504;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 128 GSYSLSVR 135
DB 156 GSYSLSVR 163
RESULT 14
LCK_CHICK STANDARD; PRT; 507 AA.
AC P42683;
DT 01-NOV-1995 (rel. 32, Created)
DT 01-NOV-1995 (rel. 32, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (Protein-
DE tyrosine kinase C-TKL).
GN LCK.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RF SEQUENCE OF 1-88 FROM N.A.
RA MEDLINE=92186854; PubMed=1545804;
RA Chow L., Ratcliffe M., Veillette A.;
RT "tkl is the avian homolog of the mammalian lck tyrosine protein
RT kinase gene.";
RT Mol. Cell. Biol. 12:1226-1233 (1992).
RN [2]
RP SEQUENCE OF 46-507 FROM N.A.
RX MEDLINE=88097370; PubMed=3321053;
RX Strebhardt K., Mullins J.I., Bruck C., Ruebsamen-Waigmann H.;
RT "Additional member of the protein-tyrosine kinase family: the src-
RT and lck-related protooncogene c-tkl.";
RT Proc. Natl. Acad. Sci. U.S.A. 84:8778-8782 (1987).
CC -1- FUNCTION: MAY PARTICIPATE IN ANTIGEN-INDUCED T-CELL ACTIVATION.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: BOUND TO THE CYTOPLASMIC DOMAIN OF EITHER
CC CD4 OR CD8.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
CC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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CC -----
DR EMBL: M85043; AAA49003.1; -
DR EMBL: J03579; AAA49081.1; ALU_INIT.
DR HSSP: P06239; 3LCK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PRINTS: PR00109; TYRKINASE.
DR Prodom: PD000001; Euk_pkinase; 1.
DR Prodom: PD000066; SH3; 1.
DR Prodom: PD000093; SH2; 1.
DR SMART: SM00252; SH2; 1.
DR SMART: SM00326; SH3; 1.
DR SMART: SM00219; TYRK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50001; SH2; 1.
DR PROSITE: PS50002; SH3; 1.
KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation; Transferase;
KW ATP-binding; Myristate; SH2 domain; SH3 domain; Palmitate;
KW Lipoprotein.
FT INIT MET 0
FT LIPID 1 1
FT LIPID 2 2
FT LIPID 4 4
FT DOMAIN 59 119
FT DOMAIN 125 222
FT SH2.

```

FT DOMAIN 243 496 PROTEIN KINASE.  
 FT NP\_BIND 249 257 ATP (BY SIMILARITY).  
 FT BINDING 271 271 ATP (BY SIMILARITY).  
 FT ACT\_SITE 362 362 BY SIMILARITY.  
 FT MOD\_RES 392 392 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT MOD\_RES 503 503 PHOSPHORYLATION (NEGATIVE REGULATION) (BY SIMILARITY).  
 SQ SEQUENCE 507 AA; 58008 MW; BC83C4FA9186170 CRC64;  
 Query Match  
 Best Local Similarity 100.0%; Score 8; DB 1; Length 507;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 128 GSYSLSVR 135  
 Db 159 GSYSLSVR 166  
 RESULT 15  
 LYN\_HUMAN STANDARD; PRT; 511 AA.  
 AC P07948;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tyrosine-protein kinase LYN (EC 2.7.1.112).  
 GN LYN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87127210; PubMed=3561390;  
 RA Yamashita Y., Fukushima S.-I., Samba K., Shikigawa J., Miyajima N.,  
 Matsubara K.-I., Yamamoto T., Toyoshima K.;  
 RT "The yes-related cellular gene lyn encodes a possible tyrosine kinase  
 RT similar to p56lck.";  
 RL Mol. Cell. Biol. 7:237-243 (1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94171041; PubMed=8125304;  
 RA Rider L.G., Raben N., Miller L., Jelsema C.;  
 RT "The CDNA encoding two forms of the LYN protein tyrosine kinase are  
 RT expressed in rat mast cells and human myeloid cells.";  
 RL Gene 138:219-222 (1994).  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOPFORMS, LYN A (SHOWN HERE) AND LYN B;  
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC  
 CC SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
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 CC -----  
 DR EMBL; M16038; AAA59540.1; -;  
 DR EMBL; M79321; AAB50019.1; -;  
 DR PIR; A26719; TVHILY.  
 DR HSSP; P08631; 1A5D.  
 DR Genew; HGNC:6735; LYN.  
 DR MIM; 165120; -;  
 DR Interpro; IPR000719; Euk\_pkinase.  
 DR Interpro; IPR000980; SH2.  
 DR Interpro; IPR001452; SH3.  
 DR Interpro; IPR001245; Tyr\_pkinase.

DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 1.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR PRODOM; PD000001; Euk\_pkinase; 1.  
 DR PRODOM; PD000066; SH3; 1.  
 DR PRODOM; PD000093; SH2; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR SMART; SM00219; Tyrc; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;  
 KW Transferase; ATP-binding; Myristate; SH2 domain; SH3 domain;  
 KW Palmitate; Lipoprotein; Alternative splicing.  
 FT INIT MET 0  
 FT LIPID 1 1 1  
 FT LIPID 2 2 2  
 FT DOMAIN 62 122 SH3.  
 FT DOMAIN 128 225 SH2.  
 FT DOMAIN 246 500 PROTEIN KINASE.  
 FT NP\_BIND 252 260 ATP (BY SIMILARITY).  
 FT BINDING 274 274 ATP (BY SIMILARITY).  
 FT ACT\_SITE 366 366 BY SIMILARITY.  
 FT MOD\_RES 396 396 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT MOD\_RES 507 507 PHOSPHORYLATION (BY SIMILARITY).  
 FT VARSPIC 42  
 SQ SEQUENCE 511 AA; 58442 MW; 8419CD461204E364 CRC64;  
 Query Match  
 Best Local Similarity 100.0%; Score 8; DB 1; Length 511;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 116 GAFLRES 123  
 Db 150 GAFLRES 157  
 RESULT 16  
 LYN\_MOUSE STANDARD; PRT; 511 AA.  
 AC P25911; O62127;  
 DT 01-MAY-1992 (Rel. 22, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tyrosine-protein kinase LYN (EC 2.7.1.112).  
 GN LYN.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Scurionath; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91260688; PubMed=1710766;  
 RA Stanley E., Ralph S.J., McEwen S., Boulet I., Holtzman D.A.,  
 Lock P., Dunn A.R.;  
 RT "Alternatively spliced murine lyn mRNAs encode distinct proteins.";  
 RL Mol. Cell. Biol. 11:3399-3406 (1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91203857; PubMed=2017160;  
 RA Y.T., Bolen J.B., Ihle J.N.;  
 RT "Hematopoietic cells express two forms of lyn kinase differing by 21  
 RT amino acids in the amino terminus.";  
 RL Mol. Cell. Biol. 11:2391-2398 (1991).  
 RN [3]  
 RP SEQUENCE OF 363-431 FROM N.A.  
 RX MEDLINE=90152381; PubMed=2482828;  
 RA Wilks A.F., Kurban R.R., Hovens C.M., Ralph S.J.;

RT "The application of the polymerase chain reaction to cloning members  
 of the protein tyrosine kinase family.";  
 RT Gene 85:67-74(1989).  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, LYN A (SHOWN HERE) AND LYN B;  
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN B-LYMPHOID AND  
 CC MYELOID CELLS.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC  
 CC SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
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 CC -----  
 DR EMBL; M64508; AAA39470.1; -;  
 DR EMBL; M57696; AAA39471.1; -;  
 DR EMBL; M57697; AAA39472.1; -;  
 DR EMBL; M33426; AAA40017.1; -;  
 DR PIR; A39719; A39719.  
 DR HSSP; P08631; 1AD5.  
 DR MGD; MGI:96892; Lym.  
 DR InterPro; IPR007719; Euk\_pkinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00018; SH2; 1.  
 DR Pfam; PF00018; SH3; 1.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Euk\_pkinase; 1.  
 DR ProDom; PD000066; SH3; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR SMART; SMO0252; SH2; 1.  
 DR SMART; SMO0326; SH3; 1.  
 DR SMART; SMO0219; TyKc; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00001; SH3; 1.  
 DR PROSITE; PS00002; SH2; 1.  
 KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;  
 KW Transferase; ATP-binding; Wristate; SH2 domain; SH3 domain;  
 KW Palmitate; Lipoprotein; Alternative splicing.  
 FT INIT MET 0  
 FT LIPID 1 1 MYRISTATE (BY SIMILARITY).  
 FT LIPID 2 2 PALMITATE (BY SIMILARITY).  
 FT DOMAIN 62 122 SH3.  
 FT DOMAIN 128 225 SH2.  
 FT DOMAIN 246 500 PROTEIN KINASE.  
 FT NP BIND 252 260 ATP (BY SIMILARITY).  
 FT BINDING 274 274 ATP (BY SIMILARITY).  
 FT ACT SITE 366 366 BY SIMILARITY.  
 FT MOD\_RES 366 366 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).  
 FT MOD\_RES 507 507 PHOSPHORYLATION (BY SIMILARITY).  
 FT VARSPDLC 24 44 MISSING (IN ISOFORM LYN B).  
 FT CONFLICT 76 76 I -> F (IN REF. 2).  
 FT CONFLICT 160 160 L -> I (IN REF. 2).  
 FT CONFLICT 278 278 P -> L (IN REF. 2).  
 FT CONFLICT 390 390 V -> I (IN REF. 2).  
 FT CONFLICT 414 414 I -> F (IN REF. 3).  
 FT CONFLICT 424 424 D -> N (IN REF. 3).  
 FT CONFLICT 431 431 L -> P (IN REF. 3).  
 SQ SEQUENCE 511 AA; 38681 MW; 3935221CC9C50F0 CRC64;

Query Match 3.1%; Score 8; DB 1; Length 511;  
 Best Local Similarity 100.0%; Pred. No. 7.5;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 116 GAFLRES 123  
 Db 150 GAFLRES 157  
 RESULT 17  
 LYN\_RAT  
 ID LYN\_RAT STANDARD; PRT; 511 AA.  
 AC Q07014; Q63320;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tyrosine-protein kinase LYN (EC 2.7.1.112).  
 GN LYN.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RX MEDLINE=97442484; PubMed=9295361;  
 RX MEDLINE=94171041; PubMed=8125304;  
 RA Rider L.G., Raben N., Miller L., Jelsma C.;  
 RT "The cDNAs encoding two forms of the LYN protein tyrosine kinase are  
 RT expressed in rat mast cells and human myeloid cells.";  
 RL Gene 138:219-222(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97442484; PubMed=9295361;  
 RA Vonk's B.M., Chen H., Haleem-Smith H., Metzger H.;  
 RT "The unique domain as the site on LYN kinase for its constitutive  
 RT association with the high affinity receptor for Ige.";  
 RL J. Biol. Chem. 272:24072-24080(1997).  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, LYN A (SHOWN HERE) AND LYN B;  
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN B-LYMPHOID AND  
 CC MYELOID CELLS.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC  
 CC SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
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 DR EMBL; L14951; AAA41549.1; -;  
 DR EMBL; L14782; AAA20944.1; -;  
 DR EMBL; L14823; AAA20945.1; -;  
 DR EMBL; AF000300; AAB71344.1; -;  
 DR EMBL; AF000301; AAB71345.1; -;  
 DR EMBL; AF000302; AAB71346.1; -;  
 DR HSSP; P08631; 1AD5.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR001245; Tyr\_pkinase.

DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 1.  
 DR Pfam; PF00069; PKINASE; 1.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR Prodom; PD000001; Euk\_pkinase; 1.  
 DR Prodom; PD000066; SH3; 1.  
 DR Prodom; PD000093; SH2; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR SMART; SM00219; TYKc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;  
 KW Transferase; ATP-binding; Myristate; SH2 domain; SH3 domain;  
 KW Palmitate; Lipoprotein; Alternative splicing.  
 FT INIT\_MET 0  
 FT LIPID 1  
 FT LIPID 2  
 FT DOMAIN 62  
 FT DOMAIN 128  
 FT DOMAIN 245  
 FT NP\_BIND 252  
 FT BINDING 274  
 FT BINDING 366  
 FT ACT\_SITE 366  
 FT MOD\_RES 396  
 FT MOD\_RES 507  
 FT VARSPLIC 24  
 FT CONFLICT 230  
 FT CONFLICT 307  
 FT CONFLICT 418  
 SQ SEQUENCE 511 AA; 58529 MW; 24A2E5E229CD3ED CRC64;

Query Match 3.1%; Score 8; DB 1; Length 511;  
 Best Local Similarity 100.0%; Pred. No. 7.5;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR 116 GAFIRES 123  
 DB 150 GAFIRES 157

RESULT 18  
 FGR MOUSE  
 ID FGR\_MOUSE STANDARD; PRT; 517 AA.  
 AC P1434; O61404;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Proto-oncogene tyrosine-protein kinase FGR (EC 2.7.1.112) (P55-FGR)  
 DE (C-FGR).  
 GN FGR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]\_Taxid=10090;  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BA/20;  
 RC MEDLINE=89385605; PubMed=2674853;  
 RA Y.I.L., Willman C.L.;  
 RT Cloning of the murine c-fgr proto-oncogene cDNA and induction of  
 RT c-fgr expression by proliferation and activation factors in normal  
 RT bone marrow-derived monocytic cells.;  
 RI Oncogene 4:1081-1087 (1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C; TISSUE=Monocytic leukemia;  
 RX MEDLINE=90191719; PubMed=2179817;  
 RA King F.J., Cole M.D.;

RT "Molecular cloning and sequencing of the murine c-fgr gene";  
 RL Oncogene 5:337-344 (1990).  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC  
 CC SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
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DR EMBL; X16440; CAA34463.1; -;  
 DR EMBL; X52191; CAA36437.1; -;  
 DR PIR; A33127; A33127.  
 DR PIR; S10072; S10072.  
 DR HSSP; P00523; 2PTK.  
 DR MGD; MGI:95527; Fgr.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 1.  
 DR Pfam; PF00069; PKINASE; 1.  
 DR PRINTS; PR00401; SH3DOMAIN.  
 DR PRINTS; PR00452; SH3DOMAIN.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR Prodom; PD000001; Euk\_pkinase; 1.  
 DR Prodom; PD000066; SH3; 1.  
 DR Prodom; PD000093; SH2; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR SMART; SM00219; TYKc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS50001; SH2; 1.  
 DR PROSITE; PS50002; SH3; 1.  
 KW Transferase; Tyrosine-protein kinase; Proto-oncogene; ATP-binding;  
 KW Phosphorylation; SH2 domain; SH3 domain.  
 FT DOMAIN 65  
 FT DOMAIN 132  
 FT DOMAIN 251  
 FT NP\_BIND 257  
 FT BINDING 279  
 FT ACT\_SITE 370  
 FT ACT\_SITE 370  
 FT MOD\_RES 400  
 FT MOD\_RES 400  
 FT CONFLICT 41  
 FT CONFLICT 212  
 SQ SEQUENCE 517 AA; 58867 MW; P655BDB4510F3076 CRC64;

Query Match 3.1%; Score 8; DB 1; Length 517;  
 Best Local Similarity 100.0%; Pred. No. 7.5;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR 116 GAFIRES 123  
 DB 154 GAFIRES 161

RESULT 19  
 HCK MOUSE  
 ID HCK\_MOUSE STANDARD; PRT; 524 AA.  
 AC F08103;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tyrosine-protein kinase HCK (EC 2.7.1.112) (P56-HCK and P60-HCK)  
 DN (Hemopoietic cell kinase) (B-cell/myeloid kinase) (BMK).  
 GN HCK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OK NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE OF 22-524 FROM N.A.  
 RC STRAIN=ICR; TISSUE=Macrophage;  
 RA MEDLINE=88067781; PubMed=3684607;  
 RX Klemz M.J., Mckercher S.R., Maki R.A.;  
 RT "Nucleotide sequence of the mouse hck gene";  
 RL Nucleic Acids Res. 15:9600-9600(1987).  
 RN [2]  
 RP SEQUENCE OF 22-524 FROM N.A.  
 RX MEDLINE=88068587; PubMed=3317404;  
 RA Holtzman D.A., Cook W.D., Dunn A.R.;  
 RT "Isolation and sequence of a cDNA corresponding to a src-related gene  
 RT expressed in murine hemopoietic cells.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:8325-8329(1987).  
 RN [3]  
 RP SEQUENCE OF 1-22 FROM N.A., AND ALTERNATIVE INITIATION.  
 RX MEDLINE=91342636; PubMed=1875927;  
 RA Lock P., Ralph S., Stanley E., Boulet I., Ramsay R., Dunn A.R.;  
 RT "Two isoforms of murine hck, generated by utilization of alternative  
 RT translational initiation codons, exhibit different patterns of  
 RT subcellular localization.";  
 RL Mol. Cell. Biol. 11:4363-4370(1991).  
 CC -1- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC  
 CC RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO  
 CC CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE  
 CC DEGRANULATION PROCESS OF NEUTROPHILS.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SUBCELLULAR LOCATION: P59-HCK AND P56-HCK ARE ASSOCIATED WITH  
 CC MEMBRANES. P59-HCK IS ALSO CYTOPLASMIC.  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms, p59-HCK (shown here) and p56-  
 CC HCK; are produced by alternative initiation.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CELLS OF THE  
 CC MYELOID AND B-LYMPHOID LINEAGES.  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC  
 CC SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
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 DR EMBL: Y00487; CAA68544.1; -;  
 DR EMBL: J03023; AAA37305.1; -;  
 DR PIR: A27282; TVMSHC.  
 DR PIR: A39773; A39773.  
 DR HSSP: P08631; IAD5.  
 DR MGI: MGI:96052; HCK.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR000980; SH2.  
 DR InterPro: IPR001452; SH3.  
 DR InterPro: IPR001245; Tyr\_pkinase.  
 DR Pfam: PF00017; SH2; 1.  
 DR Pfam: PF00018; SH3; 1.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PRINTS: PR00401; SH2DOMAIN.  
 DR PRINTS: PR00452; SH3DOMAIN.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR ProDom: PD000001; Euk\_pkinase; 1.  
 DR ProDom: PD000066; SH3; 1.  
 DR ProDom: PD000093; SH2; 1.

DR SMART: SM00252; SH2; 1.  
 DR SMART: SM00326; SH3; 1.  
 DR SMART: SM00219; TyKc; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS50001; SH2; 1.  
 DR PROSITE: PS50002; SH3; 1.  
 KW Transferrase; Tyrosine-protein kinase; Phosphorylation; ATP-binding;  
 RX Myristate; SH2 domain; SH3 domain; Alternative initiation.  
 FT CHAIN 1 524  
 FT TYROSINE-PROTEIN KINASE P59-HCK.  
 FT INIT MET 22 524  
 FT DOMAIN 142 239  
 FT DOMAIN 260 513  
 FT NP BIND 266 274  
 FT BINDING 288 288  
 FT ACT SITE 379 379  
 FT LIPID 2 2  
 FT LIPID 23 23  
 FT MOD RES 409 409  
 FT MOD RES 59129 MW; DF72FD69B38C9706 CRC64;  
 SQ SEQUENCE 524 AA; 59129 MW; DF72FD69B38C9706 CRC64;  
 Query Match 3.1%; Score 8; DB 1; Length 524;  
 Best Local Similarity 100.0%; Pred. No. 7.6;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 128 GSYSLSVR 135  
 Db 176 GSYSLSVR 183  
 RESULT 20  
 HCK HUMAN STANDARD; PRT; 526 AA.  
 ID HCK HUMAN  
 AC P08631; Q96CC0; Q9H5Y5; Q9NU4; Q9UMJ5;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Tyrosine-protein kinase HCK (EC 2.7.1.112) (P59-HCK and P60-HCK)  
 DE (Hemopoietic cell kinase).  
 GN HCK.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 CC NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE OF 22-526 FROM N.A.  
 RX MEDLINE=87257942; PubMed=3496523;  
 RA Quinirell N., Lebo R., Varnus H., Bishop J.M., Pettenati M.J.,  
 RA le Beau M.M., Diaz M.O., Rowley J.D.;  
 RT "Identification of a human gene (HCK) that encodes a protein-tyrosine  
 RT kinase and is expressed in hemopoietic cells.";  
 RL Mol. Cell. Biol. 7:2267-2275(1987).  
 RN [2]  
 RP SEQUENCE OF 22-526 FROM N.A.  
 RX MEDLINE=87257943; PubMed=3453117;  
 RA Ziegler S.F., March J.D., Lewis D.B., Perlmuter R.M.;  
 RT "Novel protein-tyrosine kinase gene (hck) preferentially expressed in  
 RT cells of hemopoietic origin.";  
 RL Mol. Cell. Biol. 7:2276-2285(1987).  
 RN [3]  
 RP SEQUENCE OF 22-526 FROM N.A.  
 RC TISSUE=B-cell;  
 RA Strausberg R.;  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 22-526 FROM N.A.  
 RC TISSUE=ileal mucosa;  
 RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,  
 RA Nakajima Y., Mizuno T., Morinaga W., Tanigami A., Fujiwara T., Ono T.,  
 RA Yamada K., Fujii Y., Ozaki K., Hiroo M., Ohmori Y., Ota T., Suzuki Y.,

RA Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,  
 RA Isegai T., Sugano S.;  
 RT "NEBO human cDNA sequencing project."  
 RL Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.  
 RN [5]  
 RX MEDLINE=21638749; PubMed=11780052;  
 RA Deloukas P., Mathewes L.H., Nehurst J., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,  
 RA Bailey J., Barlow K.P., Bates K.N., Beard L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 RA Buck D., Buttrill M.D., Butler A.P., Gardner C., Carter N.P.,  
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,  
 RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Grahnam D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekesch K., Johnson C.M., Johnson D.,  
 RA Kay W.P., Kimberley A.W., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Leharajaho M.H., Leveraha W.A., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConachie L.J., McLeay K., McMurray A.A.,  
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsey H.,  
 RA Rice C.M., Rose M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,  
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
 RA Swann R.M., Symcote N., Taylor R., Tee L., Thomas J.M., Thorpe A.,  
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.W., Thorne P.,  
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilming L., Wray P.W., Hubbard T., Dublin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20."  
 RL Nature 414:865-871(2001).  
 RN [6]  
 RX MEDLINE=92241680; PubMed=1572549;  
 RC TISSUE=Spleen;  
 RA Hradecky D., Strebhardt K., Ruesamen-Waigmann H.;  
 RT "The genomic locus of the human hemopoietic-specific cell protein  
 RT tyrosine kinase (PTK)-encoding gene (HCK) confirms conservation of  
 RT exon-intron structure among human PTKs of the src family.";  
 RL Gene 113:275-280(1992).  
 RN [7]  
 RX MEDLINE=91342636; PubMed=1875927;  
 RA Lock P., Ralph S., Stanley E., Boulet I., Ramsey R., Dunn A.R.;  
 RT "Two isoforms of murine hck, generated by utilization of alternative  
 RT translational initiation codons, exhibit different patterns of  
 RT subcellular localization.";  
 RL Mol. Cell. Biol. 11:4363-4370(1991).  
 RN [8]  
 RX X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 78-526.  
 RA Sichert F., Moarefi I., Kuriyan J.;  
 RT "Crystal structure of the Src family tyrosine kinase Hck.";  
 RL Nature 385:602-609(1997).  
 RN [9]  
 RX X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 81-137.  
 RA MEDLINE=98453315; PubMed=9778343;  
 RA Arold S., O'Brien R., Franken P., Strub M.P., Hoh F., Dumas C.,  
 RA Ladoury J.E.;  
 RT "RT loop flexibility enhances the specificity of Src family SH3  
 RT domains for HIV-1 Nef.";  
 RL Biochemistry 37:14683-14691(1998).  
 RN [10]  
 RX STRUCTURE BY NMR OF 78-138.  
 RA MEDLINE=98239731; PubMed=9571048;  
 RA Horita D.A., Baldasseri D.M., Zhang W., Altieri A.S., Smithgall T.E.,  
 RA Smeiner W.H., Byrd R.A.;  
 RT "Solution structure of the human Hck SH3 domain and identification of  
 RT its ligand binding site.";  
 RL J. Mol. Biol. 278:253-265(1998).

RN [11]  
 RP STRUCTURE BY NMR OF 139-245.  
 RX MEDLINE=97263487; PubMed=9109402;  
 RA Zhang W., Smithgall T.E., Smeiner W.H.;  
 RT "Sequential assignment and secondary structure determination for the  
 RT Src homology 2 domain of hematopoietic cellular kinase.";  
 RL FEBS Lett. 406:131-135(1997).  
 CC -1 FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC  
 CC RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO  
 CC CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE  
 CC DEGRANULATION PROCESS OF NEUTROPHILS.  
 CC -1 CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1 SUBCELLULAR LOCATION: P60-HCK AND P59-HCK ARE ASSOCIATED WITH  
 CC MEMBRANES. P60-HCK IS ALSO CYTOSOLIC (BY SIMILARITY).  
 CC -1 ALTERNATIVE PRODUCTS: 2 isoforms; P60-HCK (shown here) and P59-  
 CC HCK; are produced by alternative initiation.  
 CC -1 TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CELLS OF THE  
 CC MYELOID AND B-LYMPHOID LINEAGES.  
 CC -1 SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC  
 CC SUBFAMILY.  
 CC -1 SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
 CC -1 SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
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 DR EMBL; M16591; AAA52643.1; -;  
 DR EMBL; M16592; AAA52644.1; -;  
 DR EMBL; BC014435; AAH14435.1; -;  
 DR EMBL; AK026432; BAB15482.1; -;  
 DR EMBL; AL049539; CAB75606.1; -;  
 DR EMBL; X58741; CAA1565.2; -;  
 DR EMBL; X58742; CAA1565.2; JOINED.  
 DR EMBL; X58743; CAA1565.2; JOINED.  
 DR PIR; A27812; TVH0HC.  
 DR PDB; 2HCK; 20-AUG-97.  
 DR PDB; 3HCK; 15-OCT-97.  
 DR PDB; 4HCK; 17-JUN-98.  
 DR PDB; 5HCK; 17-JUN-98.  
 DR PDB; 1AD5; 15-MAY-97.  
 DR PDB; 1BU1; 11-NOV-98.  
 DR Genew; HGNC:4840; HCK.  
 DR MIM; 142370; -;  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR000980; SH2.  
 DR InterPro; IPR001452; SH3.  
 DR InterPro; IPR002280; Ser\_thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00017; SH2; 1.  
 DR Pfam; PF00018; SH3; 2.  
 DR Pfam; PF00069; pkinase; 4.  
 DR ProDom; PD000066; SH3; 1.  
 DR ProDom; PD000093; SH2; 1.  
 DR SMART; SM00252; SH2; 1.  
 DR SMART; SM00326; SH3; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR SMART; SM00219; Tyr\_Kc; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.  
 DR PROSITE; PSS0001; SH2; 1.  
 DR PROSITE; PSS0002; SH3; 1.  
 KW Transferrase, tyrosine-protein kinase; phosphorylation; ATP-binding;  
 KW Myristate; SH2 domain; SH3 domain; Alternative initiation;  
 KW 3D-structure.  
 FT CHAIN 1 526 TYROSINE-PROTEIN KINASE P60-HCK.  
 FT CHAIN 22 526 TYROSINE-PROTEIN KINASE P59-HCK.

```

FT INIT MET 22 22 FOR ISOFORM P59-HCK.
FT DOMAIN 78 138 SH3.
FT DOMAIN 144 241 SH2.
FT DOMAIN 262 515 PROTEIN KINASE.
FT NP_BIND 268 276 ATP.
FT BINDING 290 290 ATP.
FT ACT SITE 381 381
FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
FT MOD_RES 411 23 MYRISTATE (BY SIMILARITY).
FT CONFLICT 24 24 C -> S (IN REF. 1).
FT CONFLICT 144 144 W -> R (IN REF. 4).
SQ SEQUENCE 526 AA; 5959 MW; 847877A0A641725 CRC64;

Query Match 3.1%; Score 8; DB 1; Length 526;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 GSYSLSVR 135
Db 178 GSYSLSVR 185

RESULT 21
FGR_HUMAN STANDARD; PRT; 529 AA.
AC P09769;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-JUN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Proto-oncogene tyrosine-protein kinase fgr (EC 2.7.1.112) (P55-FGR)
DE (C-FGR).
GN FGR OR SRC2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP MEDLINE=88094395; PubMed=3275868;
RA Katamine S., Notario V., Rao C.D., Miki T., Cheah M.S.C.,
RA Tironick S.R., Robbins K.C.;
RT "Primary structure of the human fgr proto-oncogene product p55c-fgr.";
RL Mol. Cell. Biol. 8:259-266(1988).
RN [2]
RP SEQUENCE FROM N.A.
RA Heath P.;
RN Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 111-416 FROM N.A.
RX MEDLINE=8706434; PubMed=3023853;
RA Nishizawa M., Semba K., Yoshida M.C., Yamamoto T., Sasaki M.,
RA Toyoshima K.;
RT "Structure, expression, and chromosomal location of the human c-fgr
RT gene";
RL Mol. Cell. Biol. 6:511-517(1986).
RN [5]
RP SEQUENCE OF 1-143 FROM N.A.
RX MEDLINE=8826220; PubMed=3330776;
RA Inoue K., Ikawa S., Semba K., Sukegawa J., Yamamoto T., Toyoshima K.;
RT "Isolation and sequencing of cDNA clones homologous to the v-fgr
RT oncogene from a human B lymphocyte cell line, IM-9.";
RL Oncogene 1:301-304(1987).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
CC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.

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CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -----
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CC -----
DR EMBL: M19722; AA52451.1; -
DR EMBL: AL031729; CAB62968.1; -
DR EMBL: BC002836; AAH02836.1; -
DR EMBL: M12724; AA52762.1; JOINED.
DR EMBL: M12719; AA52762.1; JOINED.
DR EMBL: M12720; AA52762.1; JOINED.
DR EMBL: M12721; AA52762.1; JOINED.
DR EMBL: M12722; AA52762.1; JOINED.
DR EMBL: M12723; AA52762.1; JOINED.
DR PIR: A27676; TYRUPP.
DR PIR: A28353; A28353.
DR HSSP: P06241; 1SHF.
DR Genew; HGNC:3697; FGR.
DR MIM: 164940; -
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00017; SH2_1.
DR Pfam: PF00018; SH3_1.
DR Pfam: PF00069; pkinase_1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PRINTS: PR00109; TYRKINASE.
DR Prodom: PD000001; Euk_pkinase_1.
DR Prodom: PD000066; SH3_1.
DR Prodom: PD000093; SH2_1.
DR SMART: SM00252; SH2_1.
DR SMART: SM00326; SH3_1.
DR SMART: SM00219; TYKIC_1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00109; PROTEIN KINASE TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50001; SH2_1.
DR PROSITE: PS50002; SH3_1.
DR Transferase; Tyrosine-protein kinase; Proto-oncogene; ATP-binding;
KW Phosphorylation; SH2 domain; SH3 domain.
FT DOMAIN 77 138 SH2.
FT DOMAIN 144 241 SH3.
FT DOMAIN 263 516 PROTEIN KINASE.
FT NP_BIND 269 277 ATP (BY SIMILARITY).
FT BINDING 291 291 ATP (BY SIMILARITY).
FT ACT SITE 382 382 BY SIMILARITY.
FT MOD_RES 412 412 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SEQUENCE 529 AA; 59478 MW; 6B8C1E08414E0F9C CRC64;

Query Match 3.1%; Score 8; DB 1; Length 529;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 GAFILRES 123
Db 166 GAFILRES 173

RESULT 22
FYN_MOUSE STANDARD; PRT; 533 AA.
AC P39688;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Proto-oncogene tyrosine-protein kinase fyn (EC 2.7.1.112) (P59-FYN).

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GN FYN.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
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 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91175680; PubMed=2488273;  
 RA Cooke M.P., Perlmutter R.M.;  
 RT "Expression of a novel form of the fyn proto-oncogene in  
 RT hematopoietic cells";  
 RL New Biol. 1:66-74(1989).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RA Lee C., Kim M.G., Jeon S.H., Park D.E., Park S.D., Seong R.H.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 RN (3)  
 RP PALMITOYLATION.  
 RX MEDLINE=94019312; PubMed=8413237;  
 RA Shenoy-Scaria A.M., Timson L.K., Kwong J., Shaw A.S., Lublin D.M.;  
 RT "Palmitoylation of an amino-terminal cysteine motif of protein  
 RT tyrosine kinases p56lck and p59fyn mediates interaction with  
 RL Mol. Cell. Biol. 13:6385-6392(1993).  
 RN (4)  
 RP PALMITOYLATION.  
 RX MEDLINE=95071286; PubMed=7980442;  
 RA Koegl M., Zlatkine P., Ley S.C., Courtneidge S.A., Magee A.L.;  
 RT "Palmitoylation of multiple Src-family kinases at a homologous N-  
 RT terminal motif";  
 RL Biochem. J. 303:749-753(1994).  
 RN (5)  
 RP PALMITOYLATION.  
 RX MEDLINE=97345356; PubMed=9201723;  
 RA Wolven A., Okamura H., Rosenblatt Y., Reeh M.D.;  
 RT "Palmitoylation of p59fyn is reversible and sufficient for plasma  
 RT membrane association";  
 RL Mol. Biol. Cell 8:1159-1173(1997).  
 RN (6)  
 RP MYRISTOYLATION.  
 RX MEDLINE=96251668; PubMed=8655574;  
 RA Gaugen L.K.T., Linder M.E., Shaws A.S.;  
 RT "Multiple features of the p59fyn src homology 4 domain define a motif  
 RT for immune-receptor tyrosine-based activation motif (ITAM) binding  
 RT and for plasma membrane localization";  
 RL J. Cell Biol. 133:1007-1015(1996).  
 CC -1- FUNCTION: IMPLICATED IN THE CONTROL OF CELL GROWTH.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein  
 CC tyrosine phosphate.  
 CC -1- SUBUNIT: ASSOCIATES THROUGH ITS SH3 DOMAIN, TO THE P85 SUBUNIT OF  
 CC PHOSPHATIDYLINOSITOL 3-KINASE. INTERACTS WITH THE FYN-BINDING  
 CC PROTEIN (FYN)  
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC  
 CC SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.  
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 CC -----  
 DR EMBL, M27266; AAA37644.1; -;  
 DR EMBL, U70324; AAB09568.1; -;  
 DR PIR, A44991; A44991.  
 DR HSP, P06241.1; FYN.  
 DR MGI, MGI:95602; FYN.  
 DR InterPro, IPR000719; Euk\_pkinase.  
 DR InterPro, IPR000980; SH2.  
 DR InterPro, IPR001452; SH3.

DR InterPro, IPR001245; Tyr\_pkinase.  
 DR Pfam, PF00017; SH2; 1.  
 DR Pfam, PF00018; SH3; 1.  
 DR Pfam, PF00069; pkinase; 1.  
 DR PRINTS, PR00401; SH2DOMAIN.  
 DR PRINTS, PR00452; SH3DOMAIN.  
 DR PRINTS, PR00109; TYRKINASE.  
 DR ProDom, PD000001; Euk\_pkinase; 1.  
 DR ProDom, PD000066; SH3; 1.  
 DR ProDom, PD000093; SH2; 1.  
 DR SMART, SM00252; SH2; 1.  
 DR SMART, SM00326; SH3; 1.  
 DR SMART, SM00219; Tyrc; 1.  
 DR PROSITE, PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE, PS00109; PROTEIN\_KINASE\_TYR; 1.  
 DR PROSITE, PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE, PS50002; SH3; 1.  
 DR PROSITE, PS50002; SH2; 1.  
 KW Proto-oncogene; transferase; Tyrosine-protein kinase; Phosphorylation;  
 KW ATP-binding; Myristate; SH3 domain; SH2 domain; Palmitate;  
 KW Lipoprotein.  
 FT INIT MET 0 0  
 FT LIPID 1 1  
 FT LIPID 2 2  
 FT LIPID 5 5  
 FT LIPID 142 142  
 FT DOMAIN 148 245  
 FT DOMAIN 267 520  
 FT NP\_BIND 273 281  
 FT BINDING 295 295  
 FT ACT\_SITE 386 386  
 FT MOD\_RES 416 416  
 SQ SEQUENCE 533 AA; 59926 MW; EFD703F15B2933C CRC64;  
 Query Match 3.1%; Score 8; DB 1; Length 533;  
 Best Local Similarity 100.0%; Pred. No. 7.8;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 118 FLIRESGT 125  
 DB 172 FLIRESGT 179  
 RESULT 23  
 GCP6\_HUMAN STANDARD; PRT; 1819 AA.  
 ID GCP6\_HUMAN  
 AC Q96RT7; Q9BY91; Q9UX3; Q9UX4;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Gamma-tubulin complex component 6 (GCP-6).  
 GN GCP6 OR KIA1659.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 ON NCBI\_Taxid=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.  
 RX MEDLINE=21551508; PubMed=11694571;  
 RA Murphy S.M., Preble A.M., Patel U.K., O'Connell K.L., Dias D.P.,  
 RA Moritz W., Agard D., Stules J.T., Stearns T.;  
 RT "GCP5 and GCP6: two new members of the human gamma-tubulin complex";  
 RL Mol. Biol. Cell 12:3340-3352(2001).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20057165; PubMed=10591208;  
 RA Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,  
 RA Clump M., Smith L.J., Ainscough R., Almeida J.P., Babbage A.K.,  
 RA Baguley C., Bailey U., Barlow K.F., Bates K.N., Beasley O.P.,  
 RA Bird C.P., Blakey S.E., Bridgman A.M., Buck D., Burgess J.,  
 RA Burrill W.D., Burton J., Carter C., Carter N.P., Chen Y., Clark G.,  
 RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,  
 RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,

RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,  
 RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,  
 RA Gilbert J.G.R., Goward M.E., Heathcote D.V., Griffiths M.N.D., Hall C.,  
 RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,  
 RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,  
 RA Laird G.K., Langford C.F., Leverisha M.A., Lloyd C., Lloyd D.M.,  
 RA Martyn I.D., Mashreghi-Mohammadi M., Mathews L.H., Mccann O.T.,  
 RA Mcclary J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,  
 RA Odell C.N., Pavlit R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,  
 RA Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Ross M.T.,  
 RA Scott C.E., Sehra H.K., Skuse C.D., Smalley S., Smith M.L.,  
 RA Soderlund C., Spragon L., Steward C.A., Stilson J.E., Shan R.M.,  
 RA Vaudin M., Wall M., Wallis J.M., Whiteley W.N., Willey D.L.,  
 RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,  
 RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,  
 RA Minooshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,  
 RA Shintant A., Shibuya K., Yoshitaki Y., Aoki N., Mitsuyama S.,  
 RA Roe B.A., Chen F., Chu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,  
 RA Dorman A., Fung F., Pu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,  
 RA Lewis J., Lewis S., Lin S.-P., Lon P., Malaj E., Nguyen T., Pan H.,  
 RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shauli S., Sloan D., Song L.,  
 RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,  
 RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,  
 RA Fulton R., Johnson D., Bemis G., Bentley D., Bredshaw H., Bourne S.,  
 RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,  
 RA Hinde K., Kemp K., Latreille P., Layman D., Ozeraky P., Rohlfing T.,  
 RA Schest P., Walker C., Mansley A., Wohlmann P., Pepin K., Nelson J.,  
 RA Korf I., Bedell J.A., Hillier L., Mardis E., Waterston R., Wilson R.,  
 RA Emanuel B.S., Shaik T., Kurahashi H., Salter S., Budarf M.L.,  
 RA Mcdermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,  
 RA Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyraud M., Kedra D.,  
 RA Seoussi E., Franssen I., Tapia I., Bruder C.E., O'Brien K.P.,  
 RA Wilkinson P., Bodereich A., Hartman K., Hu X., Khan A.S., Lane L.,  
 RA Tliahun Y., Wright H.;  
 RT "The DNA sequence of human chromosome 22.":  
 RL Nature 402:489-495(1999).  
 RP SEQUENCE OF 33-1819 FROM N.A. (ISOFORM 2).  
 RC TISSUE=Brain;  
 RX MEDLINE=21156230; PubMed=11258795;  
 RA Hiroawa M., Nagase T., Murahashi Y., Kikuno R., Ohara O.;  
 RT "Identification of novel transcribed sequences on human chromosome 22  
 RT by expressed sequence tag mapping.":  
 RL DNA Res. 8:1-9(2001).  
 CC -1- FUNCTION: Gamma-tubulin complex is necessary for microtubule  
 CC nucleation at the centrosome.  
 CC -1- SUBUNIT: Gamma-tubulin complex is composed of gamma-tubulin, GCP2,  
 CC GCP3, GCP4, GCP5 and GCP6.  
 CC -1- SUBCELLULAR LOCATION: Centrosome.  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2, may be  
 CC produced by alternative splicing.  
 CC -1- SIMILARITY: BELONGS TO THE GCP FAMILY.  
 CC -1- CAUTION: Ref.3 sequence differs from that shown due to frameshifts  
 CC in positions 1371 and 1758.  
 CC -----  
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 CC -----  
 CC DR EMBL; AF272887; AAK82968.1; -;  
 CC DR EMBL; AL022328; CAB63046.1; ALT SEQ.  
 CC DR EMBL; AL022328; CAB63047.1; ALT SEQ.  
 CC DR EMBL; AB051456; BAB33339.1; ALT FRAME.  
 CC Microtubules; Repeat; Alternative splicing.  
 KM DOMAIN 1027 1269 9 x 27 AA TANDDEM REPEATS.  
 FT REPEAT 1027 1053 1.  
 FT REPEAT 1054 1080 2.  
 FT REPEAT 1081 1107 3.  
 FT REPEAT 1108 1134 4.

FT REPEAT 1135 1161 5.  
 FT REPEAT 1162 1188 6.  
 FT REPEAT 1189 1215 7.  
 FT REPEAT 1216 1242 8.  
 FT REPEAT 1243 1269 9.  
 FT VARSPLIC 1724 1757 MISSING (IN ISOFORM 2).  
 FT CONFLICT 567 567 S -> L (IN REF. 3).  
 FT CONFLICT 1377 1377 A -> T (IN REF. 2 AND 3).  
 FT CONFLICT 1621 1621 L -> V (IN REF. 2).  
 SQ SEQUENCE 1819 AA; 200455 MW; 92357654434594A CRC64;  
 Query Match 3.1%; Score 8; DB 1; Length 1819;  
 Best Local Similarity 100.0%; Pred No. 24;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 170 QALVDHYS 177  
 Db 758 QALVDHYS 765  
 RESULT 24  
 NS51\_SOYBN STANDARD; PRT; 137 AA.  
 ID NS51\_SOYBN  
 AC Q05544;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Early nodulin 55-1 precursor (N-55-1) (Fragment).  
 GN ENOD55-1.  
 OS Glycine max (Soybean).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.  
 OX NCBI\_TaxID=3847;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Williams; TISSUE=Root;  
 RX MEDLINE=94003074; PubMed=8400132;  
 RA de Blank C., Mylona P., Katinakis P.C., Bisseling T., Franssen H.;  
 RT "Characterization of the soybean early nodulin cDNA clone GmENOD55.":  
 RL Plant Mol. Biol. 22:1167-1171(1993).  
 CC -1- SUBCELLULAR LOCATION: PERIBACTEROID MEMBRANE (POTENTIAL).  
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT EARLY STAGES OF NODULE  
 CC DEVELOPMENT. MAXIMAL EXPRESSION IS SEEN IN NODULES FROM 14-DAY-OLD  
 CC PLANTS AFTER WHICH LEVELS DECREASE.  
 CC -1- INDUCTION: DURING NODULATION IN LEGUME ROOTS AFTER RHIZOBIUM  
 CC INFECTION, AND AFTER RELEASE OF BACTERIA FROM THE INFECTION  
 CC THREAD.  
 CC -1- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC DR EMBL; X69156; CAA48908.1; -;  
 CC DR InterPro; IPR003245; P1cyanin\_1like.  
 CC DR Pfam; PF02298; Cn bind like; 1.  
 CC Prodom; PD003122; P1cyanin\_1like; 1.  
 CC Nodulation; Glycoprotein; Nitrogen fixation; Signal; Membrane.  
 KM NON\_TER 1 1  
 FT SIGNAL 1 1  
 FT CHAIN 1 137  
 FT DOMAIN 1 137  
 FT CARBOHYD 13 13 PLASTOCYANIN-LIKE.  
 FT CARBOHYD 51 51 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 137 AA; 14857 MW; 988DB6F89A2EBDBD CRC64;  
 Query Match 2.7%; Score 7; DB 1; Length 137;

Best Local Similarity 100.0%; Pred. No. 21;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 12 PSPSLSS 18  
Db 97 PSPSLSS 103

## RESULT 25

RSVR\_COTUA STANDARD; PRT; 157 AA.  
AC P98162;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Subgroup A Rous sarcoma virus receptors PG890 and PG950 precursor (Low density lipoprotein receptor-related protein).  
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Archaeopteryx; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Coturnix.  
NCBI\_TaxID=93934;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94006516; PubMed=8402880;  
RA Bates P., Young J.A., Varmus H.E.;  
RT "A receptor for subgroup A Rous sarcoma virus is related to the low density lipoprotein receptor";  
RL Cell 74:1043-1051(1993).  
CC -1- FUNCTION: RESPONSIBLE FOR SUSCEPTIBILITY TO THE RETROVIRUS SUBGROUP A ROUS SARCOMA VIRUS.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Probable).  
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: PG900 (SHOWN HERE) AND PG850; ARE PRODUCED BY ALTERNATIVE SPLICING.  
CC -1- SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.  
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CC -----  
DR EMBL; L22752; -; NOT\_ANNOTATED\_CDS.  
DR EMBL; L22753; -; NOT\_ANNOTATED\_CDS.  
DR HSSP; P01130; ILDR.  
DR InterPro: IPR002172; LDL\_recept\_A.  
DR Pfam: PF00057; ldl\_recept\_a.1.  
DR SMART; SM00192; LDLa; 1.  
DR PROSITE; PS01209; LDLRA\_1; FALSE\_NEG.  
DR PROSITE; PS00068; LDLRA\_2; 1.  
KW signal; Transmembrane; Alternative splicing; Receptor; Glycoprotein.  
FT SIGNAL 1 19 POTENTIAL.  
FT CHAIN 20 157 ROUS SARCOMA VIRUS RECEPTOR PG900.  
FT DOMAIN 20 102 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 103 125 POTENTIAL.  
FT DOMAIN 126 157 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 30 47 LDL-RECEPTOR CLASS A.  
FT DISULFID 37 60 BY SIMILARITY.  
FT DISULFID 54 69 BY SIMILARITY.  
FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARSPPLIC 110 120 VILCTVAVVG -> GIPCELVAVMD (IN ISOFORM PG850).  
FT VARSPPLIC 121 157 MISSING (IN ISOFORM PG850).  
FT SEQUENCE 157 AA; 16354 MW; 726BB9AD96B7A66 CRC64;  
Qy Match 2.7%; Score 7; DB 1; Length 157;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 107 LLLLPKN 113  
Db 10 LLLLPKN 16

## RESULT 26

COAE\_RHIME STANDARD; PRT; 194 AA.  
AC Q92TE9;  
DT 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Dephospho-CoA kinase (EC 2.7.1.24) (Dephosphocoenzyme A kinase).  
GN COAE OR R00004 OR SMC02790.  
OS Bacterium meliloti (Sinorhizobium meliloti).  
OC Rhizobiales; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
OC Rhizobiaceae; Sinorhizobium.  
NCBI\_TaxID=382;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1021;  
RX MEDLINE=21396507; PubMed=11481430;  
RA Capella D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S., Godie T., Goffeau A., Kahn D., Kiss E., Lelaire V., Masny D., Pohl T., Portetelle D., Puhler A., Purnelle B., Ramsberger U., Renard C., Thebaud P., Vandenberg M., Weidner S., Gallibert F.;  
RT "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).  
CC -1- FUNCTION: Catalyzes the phosphorylation of the 3'-hydroxyl group of dephosphocoenzyme A to form coenzyme A (By similarity).  
CC -1- CATALYTIC ACTIVITY: ATP + dephospho-CoA = ADP + CoA.  
CC -1- PATHWAY: Coenzyme A (CoA) biosynthesis (By similarity).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -1- SIMILARITY: Belongs to the coa family.  
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CC -----  
DR EMBL; AL591782; CAC41391.1; -;  
DR InterPro: IPR001977; Depp\_CoAkinase.  
DR Pfam: PF01121; CoAE; 1.  
DR PRODOM: PD003329; Depp\_CoAkinase; 1.  
DR TIGRFAMs; TIGR00152; UFP0038; 1.  
DR PROSITE; PS01294; COAE; FALSE\_NEG.  
KW Transferrase; Kinase; ATP-binding; Coenzyme A biosynthesis; Complete proteome.  
FT NP BIND 8 15 ATP (POTENTIAL).  
FT SEQUENCE 194 AA; 21336 MW; D26117AEAE81F69 CRC64;  
Qy Match 2.7%; Score 7; DB 1; Length 194;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 49 AELSLRL 55  
Db 63 AELSLRL 69  
RESULT 27  
COX2\_MARPO STANDARD; PRT; 251 AA.  
AC P26857;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)



RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-T-cell;  
 RX MEDLINE=95316841; PubMed=7796396;  
 RA Fernandez-Alnemir T., Litwack G., Alnemir E.S.;  
 RT "Mch2, a new member of the apoptotic Ced-3/Ice cysteine protease gene  
 RL family";  
 RL Cancer Res. 55:2737-2742(1995).  
 RP [2]  
 RP PROCESSING.  
 RC TISSUE-Lymphocytes;  
 RX MEDLINE=97059171; PubMed=890201;  
 RA Sriwastava S.M., Fernandez-Alnemir T., Zangrilli J., Robertson N.,  
 RA Armstrong R.C., Wang L., Trapani J.A., Tomaselli K.J., Litwack G.,  
 RA Alnemir E.S.;  
 RT "The Ced-3/interleukin 1beta converting enzyme-like homolog Mch6 and  
 RT the lamin-cleaving enzyme Mch2alpha are substrates for the apoptotic  
 RT mediator Cpp32";  
 RL J. Biol. Chem. 271:27099-27106(1996).  
 CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES  
 CC RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES POLY(ADP-RIBOSE)  
 CC POLYMERASE IN VITRO, AS WELL AS LAMINS. OVEREXPRESSION PROMOTES  
 CC PROGRAMMED CELL DEATH.  
 CC -1- SUBUNIT: HETERODIMER OF A 18 kDa (P18) AND A 11 kDa (P11) SUBUNIT.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: ALPHA (SHOWN HERE) AND BETA.  
 CC ARE PRODUCED BY ALTERNATIVE SPLICING. THE BETA ISOFORM DOES NOT  
 CC SEEM TO HAVE PROTEOLYTIC ACTIVITY.  
 CC -1- PTM: CLEAVAGES BY CPP32, CASPASE-8 OR -10 GENERATE THE TWO ACTIVE  
 CC SUBUNITS.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.  
 CC  
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 CC -----  
 DR EMBL; U20536; AAC50168.1; -;  
 DR EMBL; U20537; AAC50169.1; -;  
 DR HSSP; P42574; IPAN.  
 DR MEROPS; C14.005; -;  
 DR Genew; HGNC:1507; CASP6.  
 DR MIM; 601532; -;  
 DR InterPro; IPR002398; ICE.  
 DR InterPro; IPR002138; ICE\_P10.  
 DR InterPro; IPR001309; ICE\_P20.  
 DR Pfam; PF00655; ICE\_P10; 1.  
 DR Pfam; PF00656; ICE\_P20; 1.  
 DR PRINTS; PRO0376; ILBCEZYME.  
 DR SMART; SM00115; CASC; 1.  
 DR PROSITE; PS01122; CASPASE\_CYS; 1.  
 DR PROSITE; PS01121; CASPASE\_HIS; 1.  
 DR PROSITE; PS50207; CASPASE\_P10; 1.  
 DR PROSITE; PS50208; CASPASE\_P20; 1.  
 KW Hydrolyase; Thiol protease; Apoptosis; Zymogen; Alternative splicing.  
 FT PROPEP 1 23  
 FT CHAIN 24 179 CASPASE-6 SUBUNIT P18.  
 FT PROPEP 180 193  
 FT CHAIN 194 293 CASPASE-6 SUBUNIT P11.  
 FT ACT\_SITE 121 121 BY SIMILARITY.  
 FT ACT\_SITE 163 163 BY SIMILARITY.  
 FT ACT\_SITE 102 MISSING (IN ISOFORM BETA).  
 FT VARSPLIC 14 102  
 SQ SEQUENCE 293 AA; 33409 MW; BD9204E2CCE1F670 CRC64;  
 Query Match 2.7%; Score 7; DB 1; Length 293;  
 Best Local Similarity 100.0%; Pred. No. 42;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 103 KAEELL 109  
 |||||

Db 92 KAEELL 98  
 RESULT 30  
 RNHL\_MOUSE STANDARD; PRT; 301 AA.  
 AC O9CWB8;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Ribonuclease H1 large subunit (EC 3.1.26.-) (Rnase H1 large subunit).  
 GN RNASERH2 OR RNASRH1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Embryonic stem cells;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schirral L.M., Stubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barah G.,  
 RA Blake J., Boffelli D., Bojunga N., Carlini P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Guetzknecht S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Nemboer P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Stukki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsuk S.,  
 RA Hayashizaki Y.;  
 RA "Functional annotation of a full-length mouse cDNA collection";  
 RT Nature 409:685-690(2001).  
 CC -1- FUNCTION: Degrades the ribonucleotide moiety on RNA-DNA hybrid  
 CC MOLECULES. PARTICIPATES IN DNA REPLICATION (By similarity).  
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-  
 CC phosphomonoester.  
 CC -1- SIMILARITY: BELONGS TO THE RNASE H1 FAMILY. EUKARYOTIC  
 CC SUBFAMILY.  
 CC  
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 CC -----  
 DR EMBL; A001292; BAB26828.1; -;  
 DR HSSP; Q57589; IEKE.  
 DR WGD; MG1:1916974; 2400006P09R1K.  
 DR InterPro; IPR001352; RNase\_H1/H11.  
 DR InterPro; IPR004649; Rnh11.  
 DR Pfam; PF01351; RNase\_H1; 1.  
 DR TIGRFAMs; TIGR00729; Rnh11; 1.  
 KW Hydrolyase; Nuclease; Endonuclease.  
 FT ACT\_SITE 34 34 BY SIMILARITY.  
 FT ACT\_SITE 142 142 BY SIMILARITY.  
 FT ACT\_SITE 170 170 BY SIMILARITY.  
 SQ SEQUENCE 301 AA; 33541 MW; A0F92D3F1DB43BF CRC64;  
 Query Match 2.7%; Score 7; DB 1; Length 301;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 187 LKPCVL 193

Db 25 LKPCVL 31

RESULT 31  
OGGI\_HUMAN STANDARD; PRT; 345 AA.  
AC O15527; O00390; P78554; O00670; O00705; O14876; O95488; Q9U134;  
AC Q9Y6C3; Q9Y6C4; Q9U1K0; Q9U1K1; Q9U1K2; Q9Y2C0; Q9Y2C1;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE N-glycosylase/DNA lyase [includes: 8-oxoguanine DNA glycosylase  
DE (EC 3.2.2.-); DNA (apurinic or apyrimidinic site) lyase  
DE (EC 4.2.99.18) (AP lyase)].  
GN OGG1 OR MMH OR MUTM OR OGH1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RC TISSUE=Colon;  
RX MEDLINE=97330655; PubMed=9187114;  
RA Aburatani H., Hippo Y., Ishida T., Takashima R., Matsuda C.,  
RA Kodama T., Takao M., Yasui A., Yamamoto K., Asano M., Fukasawa K.,  
RA Yoshinari T., Inoue H., Otsuka E., Nishimura S.;  
RT "Cloning and characterization of mammalian 8-hydroxyguanine-specific  
RT DNA glycosylase/apurinic, apyrimidinic lyase, a functional mutM  
RT homologue.";  
RL Cancer Res. 57:2151-2156(1997).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 1A).  
RX MEDLINE=97352815; PubMed=9207108;  
RA Rosenquist T.A., Zharkov D.O., Grollman A.P.;  
RT "Cloning and characterization of a mammalian 8-oxoguanine DNA  
RT glycosylase.";  
RL Proc. Natl. Acad. Sci. U.S.A. 94:7429-7434(1997).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 2).  
RX MEDLINE=97368311; PubMed=9223306;  
RA Roldan-Arjona T., Wei Y.-F., Carter K.C., Klungland A., Anselmino C.,  
RA Wang R.-P., Augustus M., Lindahl T.;  
RT "Molecular cloning and functional expression of a human cDNA encoding  
RT the antitumor enzyme 8-hydroxyguanine-DNA glycosylase.";  
RL Proc. Natl. Acad. Sci. U.S.A. 94:8016-8020(1997).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM 1A).  
RX MEDLINE=97368310; PubMed=9223305;  
RA Radicella J.P., Dherin C., Desmaze C., Fox M.S., Boiteux S.;  
RT "Cloning and characterization of hOGG1, a human homolog of the OGG1  
RT gene of *Saccharomyces cerevisiae*.";  
RL Proc. Natl. Acad. Sci. U.S.A. 94:8010-8015(1997).  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM 1A).  
RX MEDLINE=97342862; PubMed=9197244;  
RA Lu R., Nash H.M., Verdine G.L.;  
RT "A mammalian DNA repair enzyme that excises oxidatively damaged  
RT guanine maps to a locus frequently lost in lung cancer.";  
RL Curr. Biol. 7:397-407(1997).  
RN [6]  
RP SEQUENCE FROM N.A. (ISOFORM 1A).  
RX MEDLINE=97334205; PubMed=9190902;  
RA Axel K., Morishita K., Shimura K., Kohno T., Tanigaki M., Ohnada S.,  
RA Yokota J.;  
RT "Cloning of a human homolog of the yeast OGG1 gene that is involved in  
RT the repair of oxidative DNA damage.";  
RL Oncogene 14:2857-2861(1997).  
RN [7]  
RP SEQUENCE FROM N.A. (ISOFORM 1A).  
RX MEDLINE=98012228; PubMed=9348312;  
RA Kuo F.-C., Sklar J.L.;  
RT "Augmented expression of a human gene for 8-oxoguanine DNA glycosylase  
RT (mutM) in B lymphocytes of the dark zone in lymph node germinal  
RT centers.";  
RL J. Exp. Med. 186:1547-1556(1997).  
RN [8]  
RP SEQUENCE FROM N.A. (ISOFORM 1A).  
RX MEDLINE=98026907; PubMed=9321410;  
RA Bjoras M., Luna L., Johnsen B.E., Hoff E., Haug T., Rognes T.,  
RA Seeborg E.;  
RT "Opposite base-dependent reactions of a human base excision repair  
RT enzyme on DNA containing 7,8-dihydro-8-oxoguanine and abasic sites.";  
RL EMBO J. 16:6314-6322(1997).  
RN [9]  
RP SEQUENCE FROM N.A. (ISOFORM 1A).  
RA Dhenaut A., Boiteux S., Radicella J.;  
RT "Genomic structure and promoter characterization of the human 8-OH-  
RT guanine glycosylase gene (OGG1) gene.";  
RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.  
RN [10]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE=99380087; PubMed=10449904;  
RA Ishida T., Hippo Y., Nakahori Y., Matsushita I., Kodama T.,  
RA Nishimura S., Aburatani H.;  
RT "Structure and chromosome location of human OGG1.";  
RL Cytogenet. Cell Genet. 85:232-236(1999).  
RN [11]  
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.  
RX MEDLINE=99250167; PubMed=10233168;  
RA Nishioka K., Ohtsubo T., Oda H., Fujiwara T., Kang D., Sugimachi K.,  
RA Nakabeppu Y.;  
RT "Expression and differential intracellular localization of two major  
RT forms of human 8-oxoguanine DNA glycosylase encoded by alternatively  
RT spliced OGG1 mRNAs.";  
RL Mol. Biol. Cell 10:1637-1652(1999).  
RN [12]  
RP REVIEW.  
RX MEDLINE=20239648; PubMed=10775435;  
RA Boiteux S., Radicella J.P.;  
RT "The human OGG1 gene: structure, functions, and its implication in the  
RT process of carcinogenesis.";  
RL Arch. Biochem. Biophys. 377:1-8(2000).  
RN [13]  
RP VARIANT HIS-154.  
RX MEDLINE=96438755; PubMed=9765618;  
RA Shimura K., Kohno T., Kasai H., Koda K., Sugimura H., Yokota J.;  
RT "Infrequent mutations of the hOGG1 gene, that is involved in the  
RT excision of 8-hydroxyguanine in damaged DNA, in human gastric  
RT cancer.";  
RL Jpn. Cancer Res. 89:825-828(1998).  
RN [14]  
RP VARIANT GLN-46.  
RX MEDLINE=98324718; PubMed=9662341;  
RA Chevillard S., Radicella J.P., Levalois C., Lebeau J., Poupon M.F.,  
RA Oudard S., Dutrillaux B., Boiteux S.;  
RT "Mutations in OGG1, a gene involved in the repair of oxidative DNA  
RT damage, are found in human lung and kidney tumors.";  
RL Oncogene 16:3083-3086(1998).  
RN [15]  
RP CHARACTERIZATION OF VARIANT CYS-326.  
RX MEDLINE=99428653; PubMed=10497264;  
RA Dherin C., Radicella J.P., Dizdaroğlu M., Boiteux S.;  
RT "Excision of oxidatively damaged DNA bases by the human alpha-hOGG1  
RT protein and the polymorphic alpha-hOGG1 (Ser326Cys) protein which is  
RT frequently found in human populations.";  
RL Nucleic Acids Res. 27:4001-4007(1999).  
RN [16]  
RP CHARACTERIZATION OF VARIANTS GLN-46, HIS-154 AND CYS-326.  
RX MEDLINE=20368626; PubMed=10908322;  
RA Audebert M., Radicella J.P., Dizdaroğlu M.;  
RT "Effect of single mutations in the OGG1 gene found in human tumors on  
RT the substrate specificity of the OGG1 protein.";  
RL Nucleic Acids Res. 28:2672-2678(2000).  
CC -1- FUNCTION: DNA REPAIR ENZYME THAT INCISES DNA AT 8-OXOG RESIDUES.  
EXCISES 7,8-DIHYDRO-8-OXOGUANINE AND 2,6-DIAMINO-4-HYDROXY-5-N-

CC -----  
DR EMBL, U96710, AAB81132.1, -, -  
DR EMBL, Y11838, CAA72536.1, -, -  
DR EMBL, Y11731, CAA72414.1, -, -  
DR EMBL, AB000410, BAA19103.1, -, -  
DR EMBL, AF003595, AAB61340.1, -, -  
DR EMBL, U88527, AAB68614.1, -, -  
DR EMBL, U88520, AAB68615.1, -, -  
DR EMBL, Y13277, CAA73726.1, -, -  
DR EMBL, AF026691, AAB84013.1, -, -  
DR EMBL, AJ131141, CAA10351.1, -, -  
DR EMBL, AF088282, AAD11680.1, -, -  
DR EMBL, AF088282, AAD11681.1, -, -  
DR EMBL, AF088282, AAD11682.1, -, -  
DR EMBL, AB019528, BAA76635.1, -, -  
DR EMBL, AB019529, BAA76636.1, -, -  
DR EMBL, AB019530, BAA76637.1, -, -  
DR EMBL, AB019531, BAA76638.1, -, -  
DR EMBL, AB019532, BAA76639.1, -, -  
DR Genew, HGNC:8125, BAA76639.1, -, -  
DR OGG1.

Query Match 2.7%; Score 7; DB 1; Length 345;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC	014318	
AD	30-MAY-2000 (Rel. 39, Created)	
AE	30-MAY-2000 (Rel. 39, Last sequence update)	
AF	16-OCT-2000 (Rel. 40, Last annotation update)	
AG	38 kDa FK-506 binding protein homolog (FKBP38) (FK506-binding protein	
AH	8).	
AI	FKBP8 OR FKBP38.	
AJ	Homo sapiens (Human).	
AK	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AL	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AM	NCBI_Taxid=9606;	
AN	[1]	
AO	SEQUENCE FROM N.A.	
AP	MEDLINE=95369708; PubMed=7543869;	
AQ	Lam E., Martin M., Wiederricht G. ;	
AR	"Isolation of a cDNA encoding a novel human FK506-binding protein	
AS	homolog containing leucine zipper and tetratricopeptide repeat	
AT	motifs.";	
AV	Gene ID:297-302(1995).	
AW	[2]	
AX	SEQUENCE FROM N.A.	
AY	Lamedini J.E., McCreedy P.M., Skowronski E., Adamson A.W.,	
AZ	Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stillwagen S.,	
BA	Pan H., Velasco N., Do L., Regala W., Terry A., Barnes J.,	
BB	Dangman L., Poundstone P., Christensen M., Georgescu A., Avila J.,	
BC	Lu S., Attix C., Andreise T., Trankheim M., Antico-Keller G.,	
BD	Coeffield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,	
BE	Krommiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,	
BF	Kobayashi A., Olsen A.S., Carraro A.V. ;	
BG	"Sequence analysis of an 1 Mb region containing the MEPSB gene in	
BH	1912."	
BI	Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.	
BJ	- FUNCTION: HAS NO PRIASE/ROTANASE ACTIVITY.	
BK	- SUBUNIT: HOMOMULTIMERS OR HETEROMULTIMERS (POTENTIAL).	
BL	- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST LEVELS SEEN IN THE	
BM	BRAIN.	
BN	- SIMILARITY: BELONGS TO THE FKBP-TYPE PRIASE FAMILY.	
BO	- SIMILARITY: CONTAINS 3 TPR REPEATS.	
BP	-----	
BQ	This SWISS-PROT entry is copyright. It is produced through a collaboration	
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BV	entities requires a license agreement (See http://www.sdb-sib.ch/announce/	
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BX	-----	
BY	EMBL; L37033; AAB00102.1; -.	
BZ	EMBL; AC005387; AAC28753.1; -.	
CA	HSSP; P27124; IROT.	
CB	GeneW; HGNC:3724; FKBP8.	
CC	MIM; 604840; -.	
CD	InterPro; IPR001179; FKBP_PRIase.	
CE	InterPro; IPR001440; TPR.	
CF	Pfam; PF00254; FKBP_1.	
CG	Pfam; PF00515; TPR_3.	
CH	DR PROSITE; PS00453; FKBP_PRIASE_1; FALSE_NEG.	
CI	DR PROSITE; PS00454; FKBP_PRIASE_2; FALSE_NEG.	
CJ	DR PROSITE; PS50055; FKBP_PRIASE_3; 1.	
CK	TPR repeat; Repeat.	
CL	FT DOMAIN 63 147 PRIASE, FKBP-TYPE.	
CM	REPEAT 167 200 TPR 1.	
CN	FT REPEAT 218 251 TPR 2.	
CO	FT REPEAT 252 285 TPR 3.	
CP	SQ SEQUENCE 355 AA; 38408 MW; 4D94D8A52F426D8B CRC64;	
CQ		
CR		
CS		
CT		
CU		
CV		
CW		
CX		
CY		
CA		
CB		
CC		
CD		
CE		
CF		
CG		
CH		
CI		
CJ		
CK		
CL		
CM		
CN		
CO		
CP		
CQ		
CR		
CS		
CT		
CU		
CV		
CW		
CX		
CY		
CA		
CB		
CC		
CD		
CE		
CF		
CG		
CH		
CI		
CJ		
CK		
CL		
CM		
CN		
CO		
CP		
CQ		
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CS		
CT		
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CV		
CW		
CX		
CY		
CA		
CB		
CC		
CD		
CE		
CF		
CG		
CH		
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CJ		
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CL		
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CQ		
CR		
CS		
CT		
CU		
CV		
CW		
CX		
CY		
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CB		
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CE		
CF		
CG		
CH		
CI		
CJ		
CK		
CL		
CM		
CN		

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RESULT 33
FKBP_MOUSE STANDARD; PRT; 355 AA.
ID FKBP_MOUSE
AC 035465;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 38 kDa FK-506 binding protein homolog (FKBP38) (FK506-binding protein
8) (mukBP38)
GN FKBP8 OR FKBP38 OR SAM11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxId=10090;
RX MEDLINE=99211287; PubMed=10197430;
RA Pedersen K.W., Finsen B., Cells J.E., Jensen N.A.;
RT "mufBP38: a novel murine immunophilin homolog differentially
expressed in Schwannoma cells and central nervous system neurons in
vivo.";
RL Electrophoresis 20:249-255(1999).
CC -1- FUNCTION: HAS NO PHASE/ROTAMASE ACTIVITY (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PHASE FAMILY.
CC -1- SIMILARITY: CONTAINS 3 TPR REPEATS.
-----
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-----
DR EMBL; AF030635; AA86422.1; -.
DR HSSP; P27124; IROT.
DR MGD; MG1:1341070; FKBP8.
DR InterPro; IPR001179; FKBP_PPIase.
DR InterPro; IPR001440; TPR.
DR Pfam; PF00254; FKBP; 1.
DR Pfam; PF00515; TPR; 2.
DR PROSITE; PS00453; FKBP_PPIASE_1; FALSE NEG.
DR PROSITE; PS00454; FKBP_PPIASE_2; FALSE NEG.
DR PROSITE; PS50059; FKBP_PPIASE_3; 1.
DR TPR repeat; Repeat.
KW DOMAIN
FT DOMAIN 63 147 PPIASE, FKBP-TYPE.
FT REPEAT 167 200 TPR 1.
FT REPEAT 218 251 TPR 2.
FT REPEAT 252 285 TPR 3.
SQ SEQUENCE 355 AA; 38614 MW; 3252DE061B0F3205 CRC64;

Query Match 2.7%; Score 7; DB 1; Length 355;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 35 ATVALG 41
Db 337 ATVALG 343

RESULT 34
SOXB_RHOSO STANDARD; PRT; 365 AA.
ID SOXB_RHOSO
AC P54997;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Dibenzo[1,2-b:4,5-b']diphenylene desulfurization enzyme B (EC 3.1.2.24).
GN SOXB OR DS2B.
OS Rhodococcus sp. (strain IGT58).

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OG Plasmid.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxId=1831;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=95050323; PubMed=7961424;
RA Denome S.A., Oldfield C., Nash L.J., Young K.D.;
RT "Characterization of the desulfurization genes from Rhodococcus sp.
strain IGT58.";
RL J. Bacteriol. 176:6707-6716(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9601556; PubMed=7574582;
RA Piddington C.S., Kovacevich B.R., Rambosek J.;
RT "Sequence and molecular characterization of a DNA region encoding the
RT dibenzothiophene desulfurization operon of Rhodococcus sp. strain
RT IGT58.";
RL Appl. Environ. Microbiol. 61:468-475(1995).
CC -1- FUNCTION: PART OF A PATHWAY TO REMOVE COVALENTLY BOUND SULFUR FROM
CC DIBENZOTHIOPHENE (DBT) WITHOUT BREAKING CARBON-CARBON BONDS. THIS
CC ENZYME METABOLIZES DBT-SULFONE (DBT02 OR DBT 5,5-DIOXIDE) TO 2-
CC HYDROXYBIPHENYL (2-HBP).
CC -1- CATALYTIC ACTIVITY: 2-(2-hydroxyphenyl)benzenesulfinate + H(2)O =
CC 2-hydroxybiphenyl + sulfite.
CC -1- COFACTOR: FMN (POTENTIAL).
CC -1- PATHWAY: SECOND STEP IN PATHWAY FROM DBT TO 2-HBP.
CC -1- SUBUNIT: HETERODIMER OF TWO SUBUNITS, SOXA AND SOXB.
CC -1- SIMILARITY: BELONGS TO THE NTA/SNAA/DSZA(SOXA) FAMILY OF
CC MONOOXYGENASES.
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-----
DR EMBL; U08850; AAA6672.1; -.
DR EMBL; L37363; AAA99483.1; -.
KW Hydrolase; Monooxygenase; Flavoprotein; FMN; Plasmid.
SQ SEQUENCE 365 AA; 39044 MW; DA6A86756DA23D6 CRC64;

Query Match 2.7%; Score 7; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 236 LISEGLR 242
Db 78 LISEGLR 84

RESULT 35
HMPA_VITBPA STANDARD; PRT; 394 AA.
ID HMPA_VITBPA
AC P40609;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Flavohemoprotein (Hemoglobin-like protein) (Flavohemoglobin).
GN HMP.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxId=670;
RN (1)
RP SEQUENCE FROM N.A.
RX STRAIN=BB22;
RA McCarter L.L.;
RT Submitted (APR-1994) to the EMBL/Genbank/DBJ databases.
RL -1- DOMAIN: CONSISTS OF TWO DISTINCT DOMAINS; ONE IS A HEME-CONTAINING
CC OXYGEN BINDING DOMAIN IN THE N-TERMINAL REGION AND THE OTHER IS AN
CC FAD-CONTAINING REDUCTASE DOMAIN FOUND IN THE C-TERMINAL REGION.

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CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY. TWO-DOMAIN
CC FLAVOHEMOPROTEIN SUBFAMILY.
CC -1- SIMILARITY: TO A NUMBER OF FAD/NAD(P) FLAVOPROTEIN
CC OXIDOREDUCTASES.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U09005; AAA62190.1; -.
CC HSSP: P04252; 1VHB.
CC InterPro: IPR001834; Cyt B5 reductase.
CC InterPro: IPR000971; Globin.
CC InterPro: IPR001433; Oxid. FAD/NAD(P).
CC Pfam: PF00042; Globin. 1.
CC Pfam: PF00175; NAD binding. 1.
CC Pfam: PF00970; FAD binding. 6; 1.
CC PROSITE: PS01033; GLOBIN. 1.
CC Oxidoreductase; NADP; Heme; Flavoprotein; FAD; Iron transport;
CC Oxygen transport; Transport.
CC METAL 53 136 GLOBIN.
CC METAL 53 136 IRON (HEME DISTAL LIGAND)
CC METAL 85 85 IRON (HEME PROXIMAL LIGAND)
CC METAL 85 85 (BY SIMILARITY).
CC NP BIND 268 273 NADP (RIBOSE PART) (BY SIMILARITY).
CC SO SEQUENCE 394 AA; 44352 MW; 2AA8BA711C1A087E CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 SLSSSVQ 21
|||
207 SLSSSVQ 213

Db 207 SLSSSVQ 213

RESULT 36
ZFP38_HUMAN STANDARD; PRT; 473 AA.
ID ZFP38_HUMAN
AC Q9Y5A6; Q9H0B5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Zinc finger protein zfp-38 (NY-REN-21 antigen).
GN ZFP38.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21154917; PubMed=11230166;
RX TISSUE=Testis;
RA Wiemann S., Weil B., Mellenreuther R., Gassenhuber J., Giasel S.,
RA Ansgorge W., Boecker M., Bloeker H., Bauesachs S., Blum H.,
RA Luber J., Duesterhoeft A., Beyer A., Koerner K., Strack N.,
RA Mewes H.-W., Oltersweider B., Obermaler B., Tampe J., Heubner D.,
RA Wambutt R., Korn B., Klein M., Poustka A.;
RT "Towards a catalog of human genes and proteins: sequencing and
RT analysis of 500 novel complete protein coding human cDNAs";
RL Genome Res. 11:422-435(2001).

RN [2]
RP SEQUENCE OF 62-473 FROM N.A.
RC TISSUE=Renal cell carcinoma;
RX MEDLINE=99438124; PubMed=10508479;
RA Scanlan M.J., Gordon J.D., Williamson B., Stockert E., Bander N.H.,
RA Jongeneel V., Gure A.O., Jager D., Jager E., Knuth A., Chen Y.-T.,
RA Old L.J.;

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RT "Antigens recognized by autologous antibody in patients with renal-
RT cell carcinoma.";
RT Int. J. Cancer 83:456-464(1999).
CC -1- FUNCTION: STRONG TRANSCRIPTIONAL ACTIVATOR (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -1- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
CC FINGER PROTEINS.
CC -1- SIMILARITY: CONTAINS 1 SCAN BOX.
CC -----
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CC -----
CC EMBL: AL36865; CAB6799.1; -.
CC EMBL: AF155100; AAD4866.1; -.
CC HSSP: P08153; 1ZPD.
CC InterPro: IPR003309; Treg_SCAN.
CC InterPro: IPR000822; Znf_C2H2.
CC Pfam: PF00096; Zf_C2H2; 14.
CC Pfam: PF02023; SCAN; 2.
CC PRINTS: PR00048; ZINC_FINGER.
CC ProDom: PD000003; Znf_C2H2; 7.
CC SMART: SM00431; LER; 1.
CC SMART: SM00355; ZNF_C2H2; 7.
CC PROSITE: PS08004; SCAN_BOX; 1.
CC PROSITE: PS00028; ZINC_FINGER_C2H2_1; 6.
CC PROSITE: PS0157; ZINC_FINGER_C2H2_2; 7.
CC Zinc-finger; Metal-binding; DNA-binding; Nuclear protein; Repeat;
CC Transcription regulation; Activator.
CC METAL 45 127 SCAN_BOX.
CC METAL 277 466 ZINC_FINGERS.
CC METAL 277 299 C2H2-TYPE.
CC ZN_FING 305 327 C2H2-TYPE.
CC ZN_FING 333 354 C2H2-TYPE.
CC ZN_FING 360 382 C2H2-TYPE.
CC ZN_FING 388 410 C2H2-TYPE.
CC ZN_FING 416 438 C2H2-TYPE.
CC ZN_FING 444 466 C2H2-TYPE.
CC SO SEQUENCE 473 AA; 53658 MW; D9A26694B114B96F CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 145 IRRYRIH 151
|||||
376 IRRYRIH 382

Db 376 IRRYRIH 382

RESULT 37
HETM_ANASP STANDARD; PRT; 506 AA.
ID HETM_ANASP
AC P37693; Q44211;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Polyketide synthase hetm.
GN HETM OR AUK5357.
OS Anabaena sp. (Strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=94209228; PubMed=8157596;
RX Black T.A., Wolk C.P.;
RT "Analysis of a Het- mutation in Anabaena sp. strain PCC 7120
RT implicates a secondary metabolite in the regulation of heterocyst
RT spacing.";
RL J. Bacteriol. 176:2282-2292(1994).

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RN [2]
RP SEQUENCE FROM N.A.
RA Bauer C.C., Ramaswamy K.S., Endley S., Golden J.W., Haselkorn R.;
RL Submitted (DEC-1993) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA MEDLINE=2159285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kurita T., Saemoto S.,
RA Watanabe A., Iritani M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Rep. 8:205-213 (2001).
CC -1- COFACTOR: CONTAINS 1 COVALENTLY BOUND PHOSPHOPANTHETHEINE (BY
CC SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 ACYL CARRIER DOMAIN.
CC -----
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CC -----
CC EMBL: L22883; AAA22001.1; -.
CC EMBL: U04436; AAA03658.1; -.
CC EMBL: AP003599; BAB7056.1; -.
CC InterPro: IPR003880; Ppanche_attach.
CC DR Pfam: PF00550; pp-binding; 1.
CC DR PROSITE: PS00012; PHOSPHOPANTHETHEINE; FALSE NEG.
CC DR PROSITE: PS50075; ACP DOMAIN; 1.
CC KW Antibiotic biosynthesis; Oxidoreductase; Phosphopantetheine;
CC Multifunctional enzyme; Complete proteome.
CC FT DOMAIN 12 81 ACYL CARRIER (ACP).
CC FT BINDING 44 44 PHOSPHOPANTHETHEINE (BY SIMILARITY).
CC FT CONFLICT 442 442 F -> L (IN REF. 2).
CC SQ SEQUENCE 506 AA; 5576 MW; A3940CBE3A76558 CRC64;
CC -----
Query Match 2.7%; Score 7; DB 1; Length 506;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 116 GAFIRE 122
Db 147 GAFIRE 153

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RL Oncogene 6:361-369 (1991).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
CC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -----
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CC -----
CC EMBL: X54970; CAA38714.1; -.
CC HSP: P12931; 1PKK.
CC InterPro: IPR000719; Euk_pkinase.
CC DR InterPro: IPR000980; SH2.
CC DR InterPro: IPR001452; SH3.
CC DR InterPro: IPR001245; Tyr_pkinase.
CC DR Pfam: PF00017; SH2; 1.
CC DR Pfam: PF00018; SH3; 1.
CC DR Pfam: PF00069; pkinase; 1.
CC DR PRINTS: PR00401; SH2DOMAIN.
CC DR PRINTS: PR00452; SH3DOMAIN.
CC DR PRINTS: PR00109; TYRKINASE.
CC DR PRODOM: PD000001; Euk_pkinase; 1.
CC DR PRODOM: PD000066; SH3; 1.
CC DR PRODOM: PD000093; SH2; 1.
CC DR SMART: SM00252; SH2; 1.
CC DR SMART: SM00326; SH3; 1.
CC DR SMART: SM00219; TYRCK; 1.
CC DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
CC DR PROSITE: PS00109; PROTEIN KINASE TYR; 1.
CC DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
CC DR PROSITE: PS50001; SH2; 1.
CC DR PROSITE: PS50002; SH3; 1.
CC KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;
CC Transferrase; ATP-binding; Myristate; SH3 domain; SH2 domain.
CC FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
CC FT DOMAIN 92 153 SH3.
CC FT DOMAIN 159 256 SH2.
CC FT NP_BIND 278 531 PROTEIN KINASE.
CC FT BINDING 284 292 ATP (BY SIMILARITY).
CC FT ACT_SITE 306 306 ATP (BY SIMILARITY).
CC FT MOD_RES 397 397 BY SIMILARITY.
CC FT MOD_RES 427 427 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
CC SQ SEQUENCE 544 AA; 61288 MW; 7D4181B3E7086EF CRC64;
CC -----
Query Match 2.7%; Score 7; DB 1; Length 544;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 107 LLLLPEN 113
Db 172 LLLLPEN 178

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RESULT 39
ZP38_MOUSE
ID ZP38_MOUSE STANDARD; PRT; 555 AA.
AC Q07231;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Zinc finger protein 38 (Zfp-38) (CEFN51) (Transcription factor RU49).
GN ZP38 OR ZP-38.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;

```

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BTBRTF; TISSUE=Spermatocyte;  
 RX MEDLINE=93012481; PubMed=1397691;  
 RA Noce T., Fujiwara Y., Sezaki M., Fujimoto H., Higashinakagawa T.;  
 RT "Expression of a mouse zinc finger protein gene in both spermatocytes  
 and oocytes during meiosis";  
 RL Dev. Biol. 153:356-367(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RX MEDLINE=93183757; PubMed=1284028;  
 RA Chowdhury K.;  
 RT "The ubiquitous transactivator Zfp-38 is upregulated during  
 spermatogenesis with differential transcription.";  
 RL Mech. Dev. 39:129-142(1992).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=96189345; PubMed=8625807;  
 RA Yang X.W., Zhong R., Heintz N.;  
 RT "Granule cell specification in the developing mouse brain as defined  
 by expression of the zinc finger transcription factor Rb49.";  
 RL Development 122:555-566(1996).  
 CC -1- FUNCTION: STRONG TRANSCRIPTIONAL ACTIVATOR. ASSOCIATED WITH  
 MEIOSIS IN BOTH MALE AND FEMALE GAMETOGENESIS. MAY HAVE DIFFERENT  
 FUNCTIONS IN SOMATIC CELLS.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- TISSUE SPECIFICITY: PREDOMINANTLY IN THE SPERMATOCYTES AND  
 SPERMATIDS OF ADULT TESTES. IT IS ALSO PRESENT AT LOWER LEVELS IN  
 THE OVARY, BRAIN, SPLEEN, EMBRYO AND FETUS.  
 CC -1- DEVELOPMENTAL STAGE: FIRST DETECTED BETWEEN 2 AND 3 WEEKS AFTER  
 BIRTH. IN PARALLEL WITH THE ONSET AND PROGRESSION OF MEIOSIS. IT  
 IS EXPRESSED DURING OOOGENESIS FROM THE PROPHASE STAGE OF MEIOTIC  
 PROPHASE THROUGH TO POSTMEIOTIC CELLS.  
 CC -1- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-  
 FINGER PROTEINS.  
 CC -1- SIMILARITY: CONTAINS 1 SCAN BOX.  
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 CC -----  
 DR EMBL: D10630; BAA01480.1; -;  
 DR EMBL: X63747; CA45280.1; -;  
 DR EMBL: U41671; AAB03786.1; -;  
 DR HSSP: P08045; IZNP.  
 DR MGD: MGI:99182; Zfp38.  
 DR InterPro: IPR003309; Treg\_SCAN.  
 DR InterPro: IPR000822; Znf\_C2H2.  
 DR Pfam: PF00096; zf-C2H2; 7.  
 DR Pfam: PF02023; SCAN; 1.  
 DR PRINTS: PR00048; ZINCFINGER.  
 DR PRODOM: PD000003; Znf\_C2H2; 6.  
 DR SMART: SM00431; LER; 1.  
 DR SMART: SM00355; Znf\_C2H2; 7.  
 DR PROSITE: PS00804; SCAN\_BOX; 1.  
 DR PROSITE: PS00028; ZINC\_FINGER\_C2H2\_1; 6.  
 DR PROSITE: PS00157; ZINC\_FINGER\_C2H2\_2; 7.  
 KW Zinc-finger; Metal-binding; DNA-binding; Nuclear protein; Repeat;  
 Developmental protein; Spermatogenesis; Transcription regulation;  
 Activator.  
 KW DOMAIN  
 FT 18 134 3 X 39 AA APPROXIMATE TANDEM REPEATS.  
 FT REPEAT 18 36 1-1.  
 FT REPEAT 57 95 1-2.  
 FT REPEAT 96 134 1-3.  
 FT DOMAIN 122 204 SCAN BOX.  
 FT DOMAIN 361 548 ZINC FINGERS.  
 FT ZN\_FING 359 381 C2H2-TYPE.

FT ZN\_FING 387 409 C2H2-TYPE.  
 FT ZN\_FING 415 436 C2H2-TYPE.  
 FT ZN\_FING 442 464 C2H2-TYPE.  
 FT ZN\_FING 470 492 C2H2-TYPE.  
 FT ZN\_FING 498 520 C2H2-TYPE.  
 FT ZN\_FING 526 548 C2H2-TYPE.  
 FT CONFLICT 193 193 T -> A (IN REF. 2 AND 3).  
 FT CONFLICT 216 216 N -> S (IN REF. 3).  
 FT CONFLICT 234 234 S -> P (IN REF. 3).  
 FT CONFLICT 334 347 ASLDTGSRGAEF -> PLFKTVPGRGRA (IN  
 REF. 3).  
 FT CONFLICT 401 402 N -> KV (IN REF. 3).  
 FT CONFLICT 478 478 S -> E (IN REF. 3).  
 FT CONFLICT 495 495 E -> K (IN REF. 2).  
 FT CONFLICT 507 507 F -> L (IN REF. 2).  
 FT CONFLICT 510 510 S -> N (IN REF. 2).  
 SQ SEQUENCE 555 AA; 63042 MW; C4EBBF40A149C6C6 CRC64;  
 Query Match 2.7%; Score 7; DB 1; Length 555;  
 Best Local Similarity 100.0%; Pred. No. 76;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 145 IRRYRH 151  
 DB 458 IRRYRH 464  
 RESULT 40  
 NPAL\_MOUSE  
 ID NPAL\_MOUSE STANDARD; PRT; 594 AA.  
 AC P97459;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 GN Neuronal PAS domain protein 1 (Neuronal PAS1).  
 GE NPAS1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=97165088; PubMed=9012850;  
 RA Zhou Y.-D., Barnard M., Tian H., Li X., Ring H.Z., Franke U.,  
 RA Shelton J., Richardson J., Russell D.W., McKnight S.L.;  
 RT "Molecular characterization of two mammalian bHLH-PAS domain proteins  
 selectively expressed in the central nervous system";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:713-718(1997).  
 CC -1- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER  
 BHLH PROTEIN.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (potential).  
 CC -1- TISSUE SPECIFICITY: IN BRAIN, EXCLUSIVELY NEURONAL. ALSO FOUND IN  
 SPINAL CORD.  
 CC -1- DEVELOPMENTAL STAGE: FIRST DETECTED BETWEEN EMBRYONIC DAY 15 AND  
 DAY 16.  
 CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF  
 TRANSCRIPTION FACTORS.  
 CC -1- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.  
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 CC -----  
 DR EMBL: U77967; AAB47247.1; -;  
 DR MGD: MGI:109205; Npas1.  
 DR InterPro: IPR001097; HLH\_basic.  
 DR InterPro: IPR001610; PAC.



RA Kifken L., Riles L., Taich A., Trevaaskie E., Vignati D.,  
 RA Wilcox L., Wohldman P., Vaubin M., Wilson R., Waterston R.;  
 RA Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- PM: AUTOPHOSPHORYLATED.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC CAK1 SUBFAMILY.

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DR EMBL, X71065; CA450389.1; -  
 DR EMBL, U23464; AAA64421.1; -  
 DR EMBL, U20865; AAB67392.1; -  
 DR PIR, S47901; S47901.  
 DR HSP, 063450; 1A06.  
 DR SGD, S0004238; RCK2.  
 DR InterPro, IPR000729; Euk\_pkinase.  
 DR InterPro, IPR002290; Ser\_thr\_pkinase.  
 DR Pfam, PF00069; Pkinase; 1.  
 DR ProDom, PD000001; Euk\_pkinase; 1.  
 DR SMART, SMO0220; S\_TKC; 1.  
 DR PROSITE, PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE, PS00108; PROTEIN KINASE ST; 1.  
 DR PROSITE, PS50011; PROTEIN KINASE DOM; 1.  
 DR Transferrase; Serine/threonine-protein kinase; ATP-binding;  
 KM Phosphorylation; Calmodulin-binding.  
 FT DOMAIN 163 478 PROTEIN KINASE.  
 FT NE\_BIND 169 177 ATP (BY SIMILARITY).  
 FT BINDING 201 201 ATP (BY SIMILARITY).  
 FT ACT\_SITE 313 313 BY SIMILARITY.  
 FT DOMAIN 493 506 CALMODULIN-BINDING (POTENTIAL).  
 FT CONFLICT 109 109 N -> S (IN REF. 3).  
 FT CONFLICT 188 188 H -> N (IN REF. 3).  
 FT CONFLICT 233 233 A -> V (IN REF. 3).  
 FT CONFLICT 328 328 P -> R (IN REF. 3).  
 FT CONFLICT 456 456 S -> A (IN REF. 3).  
 FT CONFLICT 569 610 DEQLQNNFQTLIDISTIIQRRKKGQENDVGPPIPSATIR  
 E -> KMSWMTKICSN (IN REF. 1).  
 SQ SEQUENCE 610 AA; 68040 MW; DFE7B95E4D23A8A CRC64.

Query Match 2.7%; Score 7; DB 1; Length 610;  
 Best Local Similarity 100.0%; Pred. No. 83;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 221 DSSLIFS 227  
 Db 514 DSSLIFS 520

RESULT 43  
 VC42\_HAIRIN STANDARD; PRT; 631 AA.  
 ID VC42\_HAIRIN  
 AC P44236;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Mu-like prophage Flumu protein gp42.  
 GN H1514.  
 OS Haemophilus influenzae.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellales;  
 OC Haemophilus.  
 OC NCBI\_TaxID=727;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Rd / KM20 / ATCC 51907;  
 RX MEDLINE=95350630; PubMed=7542800;  
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
 RA McMeekin K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
 RA Scott J.D., Shiley R., Liu L.-I., Gloddey A., Kelly J.M.,  
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedlow E., Cotton M.D.,  
 RA Uetreback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,  
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,  
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
 RA Venter J.C.;  
 RA "Whole-genome random sequencing and assembly of Haemophilus influenzae  
 RT Rd";  
 RL Science 269:496-512(1995).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (potential).  
 CC -1- SIMILARITY: TO PHAGE MU PROTEIN GP42.

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DR EMBL, U32827; AAC23167.1; -  
 DR TIGR, H1514; -  
 DR Hypothetical protein; Transmembrane; Complete proteome.  
 KM TRANSMEM 56 76 POTENTIAL.  
 FT TRANSMEM 385 405 POTENTIAL.  
 FT TRANSMEM 455 475 POTENTIAL.  
 FT TRANSMEM 495 515 POTENTIAL.  
 FT TRANSMEM 543 563 POTENTIAL.  
 SQ SEQUENCE 631 AA; 66208 MW; 34E234C986406D82 CRC64;

Query Match 2.7%; Score 7; DB 1; Length 631;  
 Best Local Similarity 100.0%; Pred. No. 86;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 168 SIQALVD 174  
 Db 140 SIQALVD 146

RESULT 44  
 PABP\_SCHPO STANDARD; PRT; 653 AA.  
 ID PABP\_SCHPO  
 AC P31209; P87135;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Polyadenylate-binding protein (Poly(A) binding protein) (PABP).  
 GN PAB1 OR PABP OR SPAC57A7.04C.  
 OS Schizosaccharomyces pombe (Fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomyces.  
 OC NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=972;  
 RX MEDLINE=21848401; PubMed=11859360;  
 RA Wood V., Williams R., Rajadream M.A., Lyne M., Lyne R., Stewart A.,  
 RA Sgouras J., Beat N., Hayles J., Baker S., Basham D., Bowman S.,  
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,  
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
 RA Holford S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jorgels K.,  
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean U.,  
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,  
 RA Rutherford K., Butler S., Saunders D., Seeger K., Sharp S.,  
 RA Skelton J., Simmonds M., Squares R., Stevens K., Taylor K.,  
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
 RA Woodward J., Volkart G., Aert R., Robben J., Gymnopoulos B.,  
 RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,  
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,  
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Punnett B.,  
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaune V., Mottier S.,  
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
 RA Lucas M., Rochet M., Galliard C., Talada V.A., Garzon A., Thode G.,  
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,  
 RA Cerruti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,  
 RT "The genome sequence of *Schizosaccharomyces pombe*."  
 RL Nature 415:871-880(2002).  
 RN [2]  
 RP SEQUENCE OF 15-628 FROM N.A.  
 RX MEDLINE=91260690; PubMed=1575426;  
 RA Burd C.G., Matunis E.L., Dreyfuss G.,  
 RT "The multiple RNA-binding domains of the mRNA poly(A)-binding protein  
 have different RNA-binding activities.";  
 RL Mol. Cell. Biol. 11:3419-3424(1991).  
 CC -1- FUNCTION: BINDS THE POLY(A) TAIL OF MRNA.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: CONTAINS 4 RNA RECOGNITION MOTIFS (RRM).  
 CC -----  
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 CC -----  
 DR EMBL: Z95396; CAB08762.1; -;  
 DR EMBL: M64603; AA35320.1; -;  
 DR PIR: A39720; DNZPPA.  
 DR HSSP: P11940; ICVJ.  
 DR InterPro: IPR002004; PABP/HECT.  
 DR InterPro: IPR005054; RNA\_rec\_mot.  
 DR Pfam: PF00076; rrm; 4.  
 DR Pfam: PF00658; PABP; 1.  
 DR SMART: SM00517; POLYA; 1.  
 DR SMART: SM00360; RRM; 4.  
 DR PROSITE: PS00102; RRM; 4.  
 DR PROSITE: PS00030; RRM\_RNP\_1; 3.  
 KW RNA-binding; Repeat.  
 FT DOMAIN 80 158 RNA-BINDING (RRM) 1.  
 FT DOMAIN 168 245 RNA-BINDING (RRM) 2.  
 FT DOMAIN 261 338 RNA-BINDING (RRM) 3.  
 FT DOMAIN 364 441 RNA-BINDING (RRM) 4.  
 FT CONFLICT 15 34 ESDVTNNNEAVESSTKREES -> MSLNSSTLSLCSNNT  
 FT CONFLICT 349 349 R -> A (IN REF. 2).  
 FT CONFLICT 518 526 TOPPAGGA -> PLUSLEVR (IN REF. 2).  
 FT SEQUENCE 653 AA; 768F5CADD9DCEFL CRC64;  
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 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;  
 OC Spermatophyta: Magnoliophyta: eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=96347400; PubMed=8756495;  
 RA Watson M.B., Malmeberg R.L.,  
 RT "Regulation of Arabidopsis thaliana (L.) Heynh Arginine decarboxylase  
 by potassium deficiency stress.";  
 RL Plant Physiol. 111:1077-1083(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=20083487; PubMed=10617197;  
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,  
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,  
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,  
 RA Moffat K.S., Cronin L.A., Shen W., Pei G., Van Aken S., Umeyam L.,  
 RA Taiton L.J., Gill U.E., Adams M.D., Carrera A.J., Creasy T.H.,  
 RA Goodman H.M., Somerville C.R., Coppenhaver G.P., Preuss D.,  
 RA Niernm W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,  
 RA Venter J.C.,  
 RT "Sequence and analysis of chromosome 2 of the plant *Arabidopsis*  
 thaliana.";  
 RL Nature 402:761-768(1999).  
 CC -1- CATALYTIC ACTIVITY: L-arginine = agmatine + CO(2).  
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE AND MAGNESIUM.  
 CC -1- PATHWAY: FIRST STEP IN ONE OF THE TWO PUTRESCINE SYNTHESIS  
 CC PATHWAYS IN PLANTS.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF ORNITHINE, DAP, AND ARGININE  
 CC DECARBOXYLASES.  
 CC -----  
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 CC -----  
 DR EMBL: U52851; AAB09723.1; -;  
 DR EMBL: AC007195; AAD6494.1; -;  
 DR InterPro: IPR000183; Decarboxylase2.  
 DR Pfam: PF00278; Orn\_DAP\_Arg\_dec1.  
 DR Pfam: PF02784; Orn\_Arg\_dec1.  
 DR PRINTS: PR01179; ODADCBXBLASE.  
 DR TIGRfam: TIGR01273; spea; 1.  
 DR PROSITE: PS00878; ODR\_DC\_2.1; 1.  
 DR PROSITE: PS00879; ODR\_DC\_2.2; 1.  
 KW Pyridoxal phosphate; Decarboxylase.  
 FT DOMAIN 320 330 SUBSTRATE-BINDING (BY SIMILARITY).  
 FT CONFLICT 452 452 S -> F (IN REF. 1).  
 FT SEQUENCE 702 AA; 8B9D1B2B2684BCAO CRC64;  
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 Query Match 2.7%; Score 7; DB 1; Length 702;  
 Best Local Similarity 100.0%; Pred. No. 95;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 45  
 SPEI\_ARATH STANDARD; PRT; 702 AA.  
 ID SPEI\_ARATH  
 AC O99164; Q38938;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DS Arginine decarboxylase 1 (EC 4.1.1.19) (ARGDC 1) (ADC 1) (ADC-O).  
 GN SPEI OR AT2G16500 OR FIP15.12.  
 OS Arabidopsis thaliana (Mouse-ear cress).

RESULT 46  
 SPEI\_BRAJU STANDARD; PRT; 702 AA.  
 ID SPEI\_BRAJU  
 AC O82475;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

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DE Arginine decarboxylase (EC 4.1.1.19) (ARGDC) (ADC) .
GN ADCL.
OS Brassica juncea (leaf mustard) (Indian mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eusteroideae II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3707;
RN [1]
RP SEQUENCE FROM N.A.
RA Mo H., Pua E.-C.;
RT "Molecular cloning of an arginine decarboxylase cDNA from mustard
RT (Brassica juncea [L.] Czern & Coss)."
RL (In) Plant Gene Register PR98-160.
CC -1- CATALYTIC ACTIVITY: L-arginine = agmatine + CO(2) .
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE AND MAGNESIUM.
CC -1- PATHWAY: FIRST STEP IN ONE OF THE TWO PUTRESCINE SYNTHESIS
CC PATHWAYS IN PLANTS.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF ORNITHINE, DAP, AND ARGININE
CC DECARBOXYLASES.
CC -----
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CC -----
CC EMBL: AF077547; AAC62017.1;
CC InterPro: IPR000183; Decarboxylase2.
CC Pfam: PF00278; Orn_DAP_Arg_dec; 1.
CC DR Pfam: PF02784; Orn_Arg_dec N; 1.
CC DR PRINTS: PR01179; ODADECRLXASE.
CC DR TIGRFAMs: TIGR01273; spea; 1.
CC DR PROSITE: PS00878; ODR_DC_2_2; 1.
CC DR PROSITE: PS00879; ODR_DC_2_2; 1.
CC DR Putrescine biosynthesis; Spermidine biosynthesis; Lyase; Magnesium;
CC Pyridoxal phosphate; Decarboxylase.
CC KW DOMAIN
CC 325 335 SUBSTRATE-BINDING (BY SIMILARITY) .
CC FT SEQUENCE 702 AA; 76187 MW; 4FF2C7A801B1B92 CRC64;
CC SQ
Query Match 2.7%; Score 7; DB 1; Length 702;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 SPSSLS 19
DB 37 SPSSLS 43
RESULT 47
SP02_ARATH STANDARD; PRT; 711 AA.
ID SP02_ARATH
AC 023141;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Arginine decarboxylase 2 (EC 4.1.1.19) (ARGDC 2) (ADC 2) (ADC-N) .
GN SP02_ARATH:AT4G34720 OR T4L20.290.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eusteroideae II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Watson M.B., Yu W., Galloway G., Malmberg R.L.;
RT "Isolation and characterization of a second arginine decarboxylase
RT cDNA from Arabidopsis."
RL (In) Plant Gene Register PR97-114.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083488; PubMed=10617198;
RA Mayer K.F.X., Schueller C., Mambrot R., Murphy G., Volckaert G.,
RA Pohl T., Duesterhoeft A., Striekema W., Entian K.-D., Terryn N.,
RA Harris B., Amorge W., Brandt P., Grivell L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermair B., Maché R., Mueller M.,
RA Kreis M., Deleney M., Puigdomenech P., Watson M., Schmidtmann T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Voe P., Hohnel J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bigham L., Robben J.,
RA Van der Schueren J., Grynoprez B., Chang Y.-J., Vandenbussche F.,
RA Breken M., Melijns I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Weizengger T., Bothe G., Ramepeter U., Hilbert H., Braum M.,
RA Holzner E., Brandt A., Peters S., Van Scaveren M., Dirse W.,
RA Moollman P., Klein Lankhorst R., Rose M., Hauf U., Koetter P.,
RA Benneiser S., Hempel S., Feldpausch M., Lambert S., Van den Daele H.,
RA De Keyser A., Buyschaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Leonard N., McIlroy K., Mayes R.,
RA Petter A., Rajandream M.A., Lyne M., Bense V., Rechemann S.,
RA Botkova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan W., Maatse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Grandenath K., Dauner D., Hertzl A.,
RA Neumann S., Agilou A., Vitale D., Liguori R., Piravandi E.,
RA Maassen O., Quigley F., Clabaud G., Muendlein A., Felber R.,
RA Schnabel S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chedorf F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Bagues M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacón D., Jesse T.,
RA Heijman L., Schwarz S., Scholler P., Heber S., Francis P., Belke C.,
RA Frishman D., Haase D., Lemcke K., Wewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastille M., Habermann K.,
RA Parnell L., Dethia N., Gnoj L., Schütz K., Huang E., Spiegel L.,
RA Sehon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stonerking T., Kalicki J., Graves T., Hamon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Mixx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Krimer J., Fulton L., Maris E., Danne M., Pegin K., Hillier L.,
RA Nelson J., Splach J., Ryan E., Andrews S., Giesel C., Layman D.,
RA Du H., Ali J., Bergloff A., Jones K., Drone K., Cotton M., Joshi C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Jordan C.,
RA Ma P., Zhong Z., Preston R., Vill D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S.,
RA Granal S., Shohdy N., Hasegawa A., Hamed A., Lodhi M., Johnson A.,
RA Chen B., Maria W., Martensen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana."
RL Nature 402:769-777 (1999) .
CC -1- CATALYTIC ACTIVITY: L-arginine = agmatine + CO(2) .
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE AND MAGNESIUM.
CC -1- PATHWAY: FIRST STEP IN ONE OF THE TWO PUTRESCINE SYNTHESIS
CC PATHWAYS IN PLANTS.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF ORNITHINE, DAP, AND ARGININE
CC DECARBOXYLASES.
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CC EMBL: AF009647; AAB72179.1;
CC EMBL: AL023094; CAA18850.1;
CC EMBL: AL161586; CAB80188.1;
CC InterPro: IPR000183; Decarboxylase2.
CC Pfam: PF00278; Orn_DAP_Arg_dec; 1.
CC DR Pfam: PF02784; Orn_Arg_dec N; 1.
CC DR PRINTS: PR01179; ODADECRLXASE.
CC DR TIGRFAMs: TIGR01273; spea; 1.
CC DR PROSITE: PS00878; ODR_DC_2_1; 1.
CC DR PROSITE: PS00879; ODR_DC_2_2; 1.

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KM Putrescine biosynthesis; Spermidine biosynthesis; Lyase; Magnesium;  
 KM Pyridoxal phosphate; Decarboxylase.  
 FT DOMAIN 331 SUBSTRATE-BINDING (BY SIMILARITY).  
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 Db 43 SPSSSS 49  
 RESULT 48  
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 AC Q14586; Q9NRJ0;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Zinc finger protein 267 (Zinc finger protein HZF2).  
 GN ZNF267.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 CX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Schaefer U., Schneider A., Neugebauer E.;  
 RT "Identification of a nitric oxide regulated kruppel-like zinc finger  
 RT protein using motif directed differential display.";  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 12-743 FROM N.A.  
 RX MEDLINE=95169271; PubMed=7865130;  
 RA Ahrink M., Aveskogh M., Hellman L.;  
 RT "Isolation of cDNA clones for 42 different Kruppel-related zinc finger  
 RT proteins expressed in the human monoblast cell line U-937.";  
 RL DNA Cell Biol. 14:125-136(1995).  
 CC -1- FUNCTION: MAY FUNCTION AS A TRANSCRIPTION FACTOR.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).  
 CC -1- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-  
 CC FINGER PROTEINS.  
 CC -1- SIMILARITY: CONTAINS 1 KRAB DOMAIN.  
 CC  
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 CC  
 DR EMBL AF220492; AA73867.1; -.  
 DR EMBL X78925; CA55525.1; -.  
 DR HSSP; P07248; IARF.  
 DR Genew; HGNC:13060; ZNF267.  
 DR MIM; 604752; -.  
 DR InterPro; IPR001909; KRAB.  
 DR InterPro; IPR000822; Znf\_C2H2.  
 DR Pfam; PF00096; zfc\_C2H2; 30.  
 DR Pfam; PF01352; KRAB; 2.  
 DR ProDom; PD000003; Znf\_C2H2; 10.  
 DR SMART; SM00349; KRAB; 1.  
 DR SMART; SM00355; Znf\_C2H2; 15.  
 DR PROSITE; PS50805; KRAB; 1.  
 DR PROSITE; PS00028; ZINC\_FINGER\_C2H2\_1; 14.  
 DR PROSITE; PS00157; ZINC\_FINGER\_C2H2\_2; 14.  
 KM Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;  
 KM Nuclear protein; Repeat.  
 FT DOMAIN 4 75 KRAB  
 FT DOMAIN 267 738 ZINC\_FINGERS.

FT ZN\_FING 267 289 C2H2-TYPE.  
 FT ZN\_FING 322 340 C2H2-TYPE (ATYPICAL).  
 FT ZN\_FING 380 402 C2H2-TYPE.  
 FT ZN\_FING 408 430 C2H2-TYPE.  
 FT ZN\_FING 436 458 C2H2-TYPE.  
 FT ZN\_FING 464 486 C2H2-TYPE.  
 FT ZN\_FING 492 514 C2H2-TYPE.  
 FT ZN\_FING 520 542 C2H2-TYPE.  
 FT ZN\_FING 548 570 C2H2-TYPE.  
 FT ZN\_FING 576 598 C2H2-TYPE.  
 FT ZN\_FING 604 626 C2H2-TYPE.  
 FT ZN\_FING 632 654 C2H2-TYPE.  
 FT ZN\_FING 660 682 C2H2-TYPE.  
 FT ZN\_FING 688 710 C2H2-TYPE.  
 FT ZN\_FING 716 738 C2H2-TYPE.  
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 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 145 IRRYRIH 151  
 Db 564 IRRYRIH 570  
 RESULT 49  
 ID TBPE\_YEAST STANDARD; PRT; 754 AA.  
 AC P40328; P40324; Q02845; Q05773;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Probable 26S protease subunit YTA6 (TAT-binding homolog 6).  
 GN YTA6 OR YPL074W OR IPE11C.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 CX NCBI\_Taxid=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288c;  
 RX MEDLINE=95274317; PubMed=7754704;  
 RA Schnall R., Mannhaupt G., Strucka R., Tauer R., Ehnlé S.,  
 RA Scharflose C., Vetterl I., Feldmann H., Tauer R., Ehnlé S.,  
 RT "Identification of a set of yeast genes coding for a novel family of  
 RT putative ATPases with high similarity to constituents of the 26S  
 RT protease complex.";  
 RL Yeast 10:1141-1155(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=S288c / AB972;  
 RX MEDLINE=97333271; PubMed=9169875;  
 RA Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansgorge W.,  
 RA Aratijo R., Aparicio A., Bartell B.G., Badcock K., Beneš V.,  
 RA Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,  
 RA Chung E., Churcher C.M., Cosser F., Davis K., Davis R.W.,  
 RA Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,  
 RA Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,  
 RA Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.,  
 RA Hunnicke-Smith S., Hyman R., Johnston M., Kaiman S., Kleine K.,  
 RA Komp C., Kuri O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,  
 RA Marthe R., Messenguy F., Mews H.-W., Mirtipati S., Noebl D.,  
 RA Mueller-Auer S., Namath A., Nentwich U., Oeffner P., Pearson D.,  
 RA Petel F.X., Pohl T.M., Purnelle D., Schaefer M., Scharfe M.,  
 RA Scherens B., Schramm S., Schroeder M., Sdicu A.M., Tettelein H.,  
 RA Uristarazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H.,  
 RA Walsh S.W., Wambut R., Wang Y., Wedler E., Wedler H., Winnett E.,  
 RA Zhong W., Zollner A., Vo D.H., Hani J.,  
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";  
 RL Nature 387:103-105(1997).  
 RN [3]  
 RP SEQUENCE OF 1-85 FROM N.A.



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RX MEDLINE=87089718; PubMed=3025612;
RA Baker H.V.;
RT "Glycolytic gene expression in Saccharomyces cerevisiae: nucleotide
RL sequence of GCRL, null mutants, and evidence for expression.";
RL Mol. Cell. Biol. 6:3774-3784(1986).
CC -1- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
CC -1- CAUTION: Ref.1 sequence differs from that shown due to a number of
CC sequencing errors that include framehifts and rearrangements.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X81071; CAA56960.1; ALT_FRAME.
DR EMBL; X81071; CAA56959.1; ALT_FRAME.
DR EMBL; U41849; AAB68264.1; -.
DR EMBL; M4145; AAB6912.1; -.
DR PIR; S6113; S6113.
DR SGD; S0005995; YTA6.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003959; AAA_ATPase_cent.
DR Pfam; PF00004; AAA_1.
DR SMART; SM00382; AAA_1.
DR PROSITE; PS00674; AAA_1.
DR ATP-binding.
FT NP_BIND 511 518 ATP (POTENTIAL).
FT CONFLICT 20 20 L -> LQL (IN REF. 3).
FT CONFLICT 85 85 D -> I (IN REF. 3).
SQ SEQUENCE 754 AA; 85299 MW; 709F33D56382336 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 SPSSSS 19
Db 120 SPSSSS 126

RESULT 50
OCT1_XENLA STANDARD; PRT; 760 AA.
AC P16143;
DT 01-APR-1990 (Rel. 14. Created)
DT 01-AUG-1991 (Rel. 19. Last sequence update)
DT 15-JUN-2002 (Rel. 41. Last annotation update)
DE Octamer-binding transcription factor 1 (OTF-1) (NF-A1) (XOCT1).
GN OCT1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=9021827; PubMed=2326173;
RA Smith D.P.; Old R.W.;
RT "Nucleotide sequence of Xenopus laevis Oct-1 cDNA.";
RL Nucleic Acids Res. 18:369-369(1990).
RN [2]
RP SEQUENCE OF 261-335 FROM N.A.
RA Schlichte J.G.; Baarends W.M.; Peterson-Maduro J.; Destré O.H.J.;
RL Submitted (FEB-1990) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS PROTEIN IS A TRANSCRIPTION FACTOR FOR SMALL NUCLEAR
CC RNA AND HISTONE H2B GENES.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE POU TRANSCRIPTION FACTOR FAMILY.
CC CLASS-2 SUBFAMILY.

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CC -1- SIMILARITY: CONTAINS 1 HOMEBOX DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X17190; CAA35051.1; -.
DR EMBL; X51819; CAA36119.1; ALT_INIT.
DR PIR; S07896; S07896.
DR HSSP; P14859; 1OCT.
DR TRANSFAC; T00642; -.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000972; Octamer-bind_TF.
DR InterPro; IPR000227; POU_domain.
DR Pfam; PF00046; homeobox_1.
DR Pfam; PF00157; pou; 1.
DR PRINTS; PR00029; OCTAMER.
DR PRINTS; PR00028; POUDOMAIN.
DR ProDom; PD000010; Homeobox; 1.
DR ProDom; PD000583; POU domain; 1.
DR SMART; SM00389; HOX_1.
DR SMART; SM00352; POU_1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00035; POU_1; 1.
DR PROSITE; PS00465; POU_2; 1.
DR PROSITE; PS00071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Transcription regulation; Activator;
KW Nucleic protein.
FT DOMAIN 298 368 POU.
FT DNAS_BIND 397 456 HOMEBOX.
SQ SEQUENCE 760 AA; 79097 MW; 706369DA9018345 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 SPSSSS 19
Db 540 SPSSSS 546

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Search completed: March 24, 2003, 16:07:23  
Job time : 21 secs

